

Oy 1 MetProSerThrAspIeuLeuNeuMetLeuLysAlaPheGluProTyrLeuGlnIleLeuGln 20
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Search completed: October 7, 2003, 07:12:07
Job time : 4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 6, 2003, 12:29:09 ; Search time 109 Seconds
(without alignments)
6912.303 Million cell updates/sec

Title: US-10-053-510-7
Perfect score: 1707
Sequence: 1 atgcctagcacagacctct.....gtctccaaaccactga 1707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1707	100.0	1707	4	US-09-356-643B-7
4	1699	99.5	2130	4	US-09-740-369-1
5	1278.2	74.9	1707	4	US-08-939-309-1
6	1278.2	74.9	1707	4	US-09-849-180-1
7	1278.2	74.9	1707	4	US-09-356-643B-5
8	1217	71.3	1467	4	US-08-939-309-9
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41	31.6	1.9	3910	4	US-09-120-653D-1	Sequence 1, Appl
42	31.6	1.9	9639	4	US-09-147-208-26	Sequence 26, Appl
43	31.6	1.9	9639	4	US-09-550-117A-26	Sequence 26, Appl
44	31.6	1.9	9690	4	US-09-182-145-55	Sequence 55, Appl
45	31.6	1.9	10241	1	US-08-508-448C-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-939-309-3
Sequence 3, Application US/08939309
Patent No. 6423527
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SHINGOSINE-1-PHOSPHATE LYASE
TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Mark J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
US-08-939-309-3
Query Match 100.0%; Score 1707; DB 4; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1681 ATGAATGATTCACAAACCCCACTGA 1707
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RESULT 2
US-09-849-180-3
Sequence 3, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Sada, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985

REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-849-180-3

Query Match 100.0%; Score 1707; DB 4; Length 1707;
Best Local Similarly 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-356-643b-7
Sequence 7, Application US/09356643b
Patent No. 659666
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR

FILE REFERENCE: 200116.402C1
CURRENT APPLICATION NUMBER: US/09/356.643B
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1707
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1707)
US-09-356-643B-7

Query Match 100.0%; Score 1707; DB 4; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGCTACACAGACCTCTGATGTTGAAGCCCTTGAGCCCTACTAGAGATTTTGGAA 60
QY 61 GATATCTCACAAAAGCCCAAGATTAATGAGCATTTGACCAAGATGAGCCCTGG 120
DB 61 GATATCTCACAAAAGCCCAAGATTAATGAGCATTTGACCAAGATGAGCCCTGG 120
QY 121 CAGCTAATTCGATGAGAGTGTGCTGTGAGCCCTGCTGATAGTCTGGGATATGAGTTGTC 180
DB 121 CAGCTAATTCGATGAGAGTGTGCTGTGAGCCCTGCTGATAGTCTGGGATATGAGTTGTC 180
QY 181 TTCCAGCCAGAGAGTTTATGCTCAAGGTTTAAAAAATGTTTAACTCACAGAGAG 240
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QY 601 GATTGCTGTGATGTGACTTCTGGGGAACAGAAACATATCATGAGCTGCAAAACA 660
DB 601 GATTGCTGTGATGTGACTTCTGGGGAACAGAAACATATCATGAGCTGCAAAACA 660
QY 661 TGTGGGAGTGTGGCCTTTGAGAAGGGGATCAAAACTCCAGAAATTTGGCTCCCAAGT 720
DB 661 TGTGGGAGTGTGGCCTTTGAGAAGGGGATCAAAACTCCAGAAATTTGGCTCCCAAGT 720
QY 721 GCCCATGCTGATTTTAACAAGCAGCCGTTACTTTGGGATGAAGATTGTGGGGTCCCA 780
DB 721 GCCCATGCTGATTTTAACAAGCAGCCGTTACTTTGGGATGAAGATTGTGGGGTCCCA 780
QY 781 TTGACAGAGATGATGAGAGTGTGAGGCAATGAGAAGAGCATATCCAGAGAACT 840
DB 781 TTGACAGAGATGATGAGAGTGTGAGGCAATGAGAAGAGCATATCCAGAGAACT 840

QY 841 GCCATGCTGCTGTTTCTACACCCACAGTTTCCATAGTGTATAGATCTCTCCCTGAA 900
DB 841 GCCATGCTGCTGTTTCTACACCCACAGTTTCCATAGTGTATAGATCTCTCCCTGAA 900
QY 901 GTGGCCAAAGCTGGCTGTCAATATCAAAATACCCCTTCATGTGACGCTTGTGGAGGC 960
DB 901 GTGGCCAAAGCTGGCTGTCAATATCAAAATACCCCTTCATGTGACGCTTGTGGAGGC 960
QY 961 TTCTCATGCTGTTTATGAGAGAAAGCAGATATCCACAGTGAACCCATTTTATTTCCGG 1020
DB 961 TTCTCATGCTGTTTATGAGAGAAAGCAGATATCCACAGTGAACCCATTTTATTTCCGG 1020
QY 1021 GTGAAGGTGTAAACAGATTTTACCTGACACCCATTAAGTATGCTATGCCCAAAAGGC 1080
DB 1021 GTGAAGGTGTAAACAGATTTTACCTGACACCCATTAAGTATGCTATGCCCAAAAGGC 1080
QY 1081 TCATCATTTGGTGTGTATATGAGCAAGAAGTACAGAACTATCATGTTCTGTGCATACA 1140
DB 1081 TCATCATTTGGTGTGTATATGAGCAAGAAGTACAGAACTATCATGTTCTGTGCATACA 1140
QY 1141 GATTGCAAGGGTGGCATCTATGCTTCCCAACCATCGCAGGCTCACGGCTGTGGCATTT 1200
DB 1141 GATTGCAAGGGTGGCATCTATGCTTCCCAACCATCGCAGGCTCACGGCTGTGGCATTT 1200
QY 1201 AGCGAGCCTGTTGGGCTGCTTGAATGACATTTGGTGAACGCTATGTTGAAGCTAAC 1260
DB 1201 AGCGAGCCTGTTGGGCTGCTTGAATGACATTTGGTGAACGCTATGTTGAAGCTAAC 1260
QY 1261 AAACAGATATCAAAACGCTGCTCTCTCAAGTACAGAACTGGAATAATCAAAAGCATTC 1320
DB 1261 AAACAGATATCAAAACGCTGCTCTCTCAAGTACAGAACTGGAATAATCAAAAGCATTC 1320
QY 1321 TTTGTTTGGGAATCCCAATTTGCTACATGCTGTGGGATCCCGTATTTGACATTC 1380
DB 1321 TTTGTTTGGGAATCCCAATTTGCTACATGCTGTGGGATCCCGTATTTGACATTC 1380
QY 1381 TACGAGTATCAAAACCTGATGACTGTAAAGGGTGAACCTTGAAACGATTTGCCATTC 1440
DB 1381 TACGAGTATCAAAACCTGATGACTGTAAAGGGTGAACCTTGAAACGATTTGCCATTC 1440
QY 1441 CCCATATTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
DB 1441 CCCATATTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
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DB 1501 CTAAAGACATTTGGAATCTGTCACTCAATCAATCAATCAATCAATCAATCAATCAAT 1560
QY 1561 GGAATGGGTGCCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 GGAATGGGTGCCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 TTTGCTCATGCTTGTGAGAGCTTGAAGAGCAGTGTGACAGCACTGTACCCAGGCGCAG 1680
DB 1621 TTTGCTCATGCTTGTGAGAGCTTGTGAGAGCAGTGTGACAGCACTGTACCCAGGCGCAG 1680
QY 1681 ATGAATGTTCTCCAAACCCCACTGA 1707
DB 1681 ATGAATGTTCTCCAAACCCCACTGA 1707

RESULT 4
US-09-740-369-1
Sequence 1, Application US/09740369
Patent No. 6521437
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID MALCOLM
APPLICANT: GODDEN, ROBERT JAMES
APPLICANT: TESFA, TANIA TAMSON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30034-D1
CURRENT APPLICATION NUMBER: US/09/740.369

Db	958	TTGACGAAGATGATGAGTGGATGATGTGGGGGCAATGAGAAGAGCTATCTCCAGAACT	1017
QY	841	GCCATGCTGTCGTGTTGTTCTAACCCACAGTTTCCTCATGCTGTAAATAGATCTGTCCCTGAA	900
Db	1018	GCCATGCTGTCGTGTTGTTCTAACCCACAGTTTCCTCATGCTGTAAATAGATCTGTCCCTGAA	1077
QY	901	GTGGCCCAAGCTGGCTGTCAAAATACAAATTACCCCTTCATGTTGAGCGCTGTCTGGGAGGC	960
Db	1078	GTGGCCCAAGCTGGCTGTCAAAATACAAATTACCCCTTCATGTTGAGCGCTGTCTGGGAGGC	1137
QY	961	TTCCGTCATCGTCTTTATGAGAAACAGAGATACCCACTGTGAGACACCCATTTGATTTCCGG	1020
Db	1138	TTCCGTCATCGTCTTTATGAGAAACAGAGATACCCACTGTGAGACACCCATTTGATTTCCGG	1197
QY	1021	GTGAAGGTGTAACCAAGCATTTTCAGCTGACACCCATTAAGTATGCTATGCCCCCAAAAGGC	1080
Db	1198	GTGAAGGTGTAACCAAGCATTTTCAGCTGACACCCATTAAGTATGCTATGCCCCCAAAAGGC	1257
QY	1081	TCATCATTTGGTGTGTATAGTGACAAAGATACAGAACTATCAGTTCTTTCGTGATACA	1140
Db	1258	TCATCATTTGGTGTGTATAGTGACAAAGATACAGAACTATCAGTTCTTTCGTGATACA	1317
QY	1141	GATTGGCAGGGGGGCGCATATGACCTTCCCAACATTCGCGACGGCTCAGCGGCTGTGGCATTT	1200
Db	1318	GATTGGCAGGGGGGCGCATATGACCTTCCCAACATTCGCGACGGCTCAGCGGCTGTGGCATTT	1377
QY	1201	AGCGCAGCGCTTGTGGGCTGCCCTTGATGACACTTCGGGTGAGAACGGCTATGTTGAAGCTACC	1260
Db	1378	AGCGCAGCGCTTGTGGGCTGCCCTTGATGACACTTCGGGTGAGAACGGCTATGTTGAAGCTACC	1437
QY	1261	AAACAGATCATCAAAACAGTGCCTGCTTCTCAAGTACAGAACTGGAATATCAAAAGCATTC	1320
Db	1438	AAACAGATCATCAAAACAGTGCCTGCTTCTCAAGTACAGAACTGGAATATCAAAAGCATTC	1497
QY	1321	TTTGTGTTTGGGAATCCCCAATGTGCACATTCGCTGCGATGCCGTGGATPCCGTCATTTTGACATC	1380
Db	1498	TTTGTGTTTGGGAATCCCCAATGTGCACATTCGCTGCGATGCCGTGGATPCCGTCATTTTGACATC	1557
QY	1381	TACCGACTATCAAAACCTGATGACTGCTTAAGGGGTGGAACCTTGAAACAGTTGACGTTCCCA	1440
Db	1558	TACCGACTATCAAAACCTGATGACTGCTTAAGGGGTGGAACCTTGAAACAGTTGACGTTCCCA	1617
QY	1441	CCCAGTATTCAATTTTGTGCATCACAATTACTACACGCCGCCGGAACGAGTACTATACAATTC	1500
Db	1618	CCCAGTATTCAATTTTGTGCATCACAATTACTACACGCCGCCGGAACGAGTACTATACAATTC	1677
QY	1501	CTAAAGGACATTCGGAATCTGTCACTCACTCAAAATCATGAAGAATCCTTAAACGGAAGACACA	1560
Db	1678	CTAAAGGACATTCGGAATCTGTCACTCACTCAAAATCATGAAGAATCCTTAAACGGAAGACACA	1737
QY	1561	GGAATGGGTGCCATTTATGCCATGTGCGCCAGACACAATCTGTGACAGAAATATGGTTGCAGAA	1620
Db	1738	GGAATGGGTGCCATTTATGCCATGTGCGCCAGACACAATCTGTGACAGAAATATGGTTGCAGAA	1797
QY	1621	TTGTGCTCAGTCTTCTTGGACAGCTTGTACACAGCACCGACACTGTCAACCCAGGCGACCGAG	1680
Db	1798	TTGTGCTCAGTCTTCTTGGACAGCTTGTACACAGCACCGACACTGTCAACCCAGGCGACCGAG	1857
QY	1681	ATGAATGGTTCCTCCAAAMCCCACTGCA 1707	
Db	1858	ATGAATGGTTCCTCCAAAMCCCACTGCA 1884	
RESULT 5			
US-08-939-309-1			
; Sequence 1, Application US/08939309			
; Patent No. 6423527			
; GENERAL INFORMATION:			
; APPLICANT: Saba, Julie D.			
; APPLICANT: Zhou, Jianhui			
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE			
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND			
; TITLE OF INVENTION: METHODS OF USE THEREFOR			

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Mark J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
US-08-939-309-1

Query Match 74.9% Score 1278.2; DB 4; Length 1707;
Best Local Similarity 84.3%; Pred. No. 0; Mismatches 268; Indels 0; Gaps 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

QY 1 ATGCGTAGCAGACGCTTGTATGTTGAAGCCCTTGAAGCCCTTATAGAGATTTTGGAA 60
DB 1 ATGCGCGGACGACGCTCTCAAGCTGAGACCTTCGAGCTTATTTAGAGATTTTGGAA 60
QY 61 GTATATCTCACAAGCCAGAAATTTATGTAATGAGACATTCACCACTATGAGCCCTGG 120
DB 61 TCTTATTCACAAAGCCAAAGATTTATGTAATGAGATATTCACCAATATGAGCCCTGG 120
QY 121 CAGCTAATTCATGAGAGTGTGTGAGACCTGCTGATAGTCTGGGGATATGATTTCTC 180
DB 121 CAGCTATTCGAGAGTGTGTGAGACCTGCTGATAGTCTGGGGATATGAGCTTATC 180
QY 181 TTCCAGCCAGAGATTTATGTTCAAGTTTAAAAAGAAATGTTTAAAGCTCACCAGAG 240
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QY 241 ATGCCCATTTATGTTGCTGTAAGATTCAGACAAGTTGAACAAGACCAGAGATATTAAC 300
DB 241 ATGCCCATTTATGTTGCTGTAAGATTCAGACAAGTTGAACAAGACCAGAGATTTTGC 300
QY 301 AAGAAGATGTCATTCCTGAAGGTGAGACAAAGATATGTAAGAGTTTCCCTCCAGAGGT 360
DB 301 AAGAAGATGTCATTCCTGAAGGTGAGACAAAGATATGTAAGAGTTTCCCTCCAGAGGT 360
QY 361 CTGAGCTCATCTGTTGTTTGGAGAAACCTTAAGAGTACAGCTCATGAGAGCCCTTGG 420
DB 361 ATGGGACAGCTGAGGTTCTGAGAGACTCAAGAGGTACAGCTCATGAGAGGTTCTGG 420
QY 421 CAAAGAGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAACTACTGAGCTCTT 480
DB 421 CAAAGAGGAGAGCCTCTGGAACAGTGTGTACAGTGGGAGAGAACTACTGAGCTCTG 480
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DB 481 GTGAAGGCTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATATCTTCCACAGA 540

DB 481 GTGACGCTTATGAGAAATTCACGTGAGACCAATCCACTGATCCAGATATCTTCCCTG 540
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DB 781 CTGAAGAAAGATGATGAGGTGATGTGAGGGCAATGAGAAAGCTATCTCCAGAACT 840
QY 841 GCCATGCTGCTGTTTACACCCAGTTTCTCATGGTATGATGATCTGCTCCCTAA 900
DB 841 GCTATGCTGTGTGTTTACACCCAGTTTCTCATGGTATGATGATCTGCTCCCTAA 900
QY 901 GTGGCAGAGCTGCTGTCAAAATATACAAATACCCCTTCAATGTGACGCTTGTCTGGAG 960
DB 901 GTGGCAGAGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 961 TTCTCATGCTGCTTATGAGAGAAAGCAGATATCCACTGAGACCCATTTGATTTCCGG 1020
DB 961 TTCTCATGCTGCTTATGAGAGAAAGCAGATATCCACTGAGACCCATTTGATTTCCGG 1020
QY 1021 GTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 GTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 TCATCATGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 TCATCATGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 GATTGGCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 GATTGGCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AGCCGAGCTGTTGGGCTGCTTATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 ATTCAGGCTGTTGGGCTGCTTATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAACAGATCATCAAAACTGCTGCTTCTCAAGTCAAGATGGAATATCAAAAGCATC 1320
DB 1261 AAACAGATCATCAAAACTGCTGCTTCTCAAGTCAAGATGGAATATCAAAAGCATC 1320
QY 1321 TTTGTTTGGGAATCCCAATTTGCTGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 TTTGTTTGGGAATCCCAATTTGCTGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 TACGACATATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
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QY 1441 CCCAGATTCATTTCTGATCATATCTACAGCCGCGGAAACGATGATACATATTC 1500
DB 1441 AGAAGCATTCATTTCTGATCATATCTACAGCCGCGGAAACGATGATACATATTC 1500
QY 1501 CTAAGGATATTCGAGATCTGTCTCAATCATGAGGATTCCTAAAGCGAAGCCACA 1560
DB 1501 CTAAGGATATTCGAGATCTGTCTCAATCATGAGGATTCCTAAAGCGAAGCCACA 1560
QY 1561 GGAATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 GGAATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620

QY 1621 TTCCTCAGCTTCTTGGACAGCTTGACAGCACCAGACTGTACACCCAGGCGACCCAG 1680
1621 ATATCCTCCGCTCTTCTGACCTCTTACTACAGGACCCCGTGTACAGGCAACAG 1680
QY 1681 ATGAATGTTTCCAAACCCACCTGA 1707
1681 ATGACGGTCTCCAAACCCCGCTGA 1707
Db 1681 ATGACGGTCTCCAAACCCCGCTGA 1707
RESULT 6
US-09-849-180-1
Sequence 1, Application US/09849180
Patent No. 6493359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4800
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-180-1
Query Match 74.9%; Score 1278.2; DB 4; Length 1707;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1459; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

Db 181 TTCACGACAGAGTTTATGTCCTCGTTTAAAAAATAATATTAAAGCTTATCAGGAAG 240
QY 241 ATGCCCATTTTGTGTGTAAGATTCAAGACAGAGTTGAACAGCAAGAGATATTAGC 300
241 ATGCCATTTTGTGTGAGCTTAAGATCGAACACAGAGTGAACAGCAAGAGATCTTGTG 300
QY 301 AAGACATGTCATCTTCTGAAGAGTGACAAAGATATGTAAGCTTTTACCCTCCAGGT 360
301 AAGACATGTCATCTTCTGAAGAGTGACAAAGATATGTAAGCTTTTACCCTCCAGGT 360
Db 301 AAGACATGTCATCTTCTGAAGAGTGACAAAGATATGTAAGCTTTTACCCTCCAGGT 360
QY 361 CTGAGCTCATCTCTGTTTGGAGAACTTAAGAGTACAGCTGTATGACGCTTCTGG 420
361 ATGGGACACAGCTGAGGTTCTGGAGAGACTCAAGAGATACAGCTCATGATGATGCTTGG 420
QY 421 CAAGAGGGAGAGCTCTGACAGAGTACAGTACAGTGGGAGGAGAAAGCTACAGCTCTT 480
421 CAAGAGGGAGAGCTCTGACAGAGTACAGTACAGTGGGAGGAGAAAGCTACAGCTCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGTGATGAGTACCCCTCGCATCCAGATATCTTCCAGGA 540
481 GTGACAGCTTATGAGATTTTGTGATGAGTACCCCTCGCATCCAGATATCTTCCAGGA 540
QY 541 CTACGCAAGATTAAGGACAGAAATTTGAGATAGCTTGTCTTCAATGGGAGCCA 600
541 TTGCGGAAATTAGAGGACAGAAATCTTACAGTACCTTCCCTCAATGGGAGCCA 600
QY 601 GATTGCGATGATGTGACTTCTGGGGGAAAGAAAGCATATCAGTGGGCTGCAAGCA 660
601 GATTGCTGATGATGTGACTTCTGGGGGAAAGAAAGCATATCAGTGGGCTGCAAGCA 660
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661 TACCGGAGCTTGTGCGTGAAGAGGGGATCAAAACTCCAGAAATTTGTGCTCCCAAGT 720
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721 GCCCATGCTCATTTAACAAGACGACAGTACTTTGGATGAAGATTTGGCGGCTCCA 780
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781 TTGACGAAATGATGAGGATGATGAGGAGCAATGAGAGAGCTATCTCAGGAACACT 840
Db 781 TTGACGAAATGATGAGGATGATGAGGAGCAATGAGAGAGCTATCTCAGGAACACT 840
QY 841 GCCATGCTGCTGCTTCTACCCCAAGATTTCTCATGCTGTAATAGATCTGCTCCGAA 900
841 GCTATGCTGCTGCTTCTACCCCAAGATTTCTCATGCTGTAATAGATCTGCTCCGAA 900
QY 901 GTGGCCAGCTGCTGCTCAATTAACAAATTAACCCCTTCAATGTCAGAGCTGTCTGGAGGC 960
901 GTGGCCAGCTGCTGCTCAATTAACAAATTAACCCCTTCAATGTCAGAGCTGTCTGGAGGC 960
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961 TTCCTCATGCTCTTTATGGAAGAGAGATGATGAGGATGAGGAGGATGAGGATGAGG 1020
Db 961 TTCCTCATGCTCTTTATGGAAGAGAGATGATGAGGATGAGGAGGATGAGGATGAGG 1020
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1021 GTGAAGAGTGTGTAAACAGCATTTGAGTGAACAGCATTGATGAGTGTGAGGATGAGG 1080
Db 1021 GTGAAGAGTGTGTAAACAGCATTTGAGTGAACAGCATTGATGAGTGTGAGGATGAGG 1080
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1081 TCATCATGCTGCTGCTGATGATGACAGAGTACAGAGATTAAGTATGCTGCTGATGA 1140
Db 1081 TCATCATGCTGCTGCTGATGATGACAGAGTACAGAGATTAAGTATGCTGCTGATGA 1140
QY 1141 GATTGAGGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
1141 GATTGAGGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
Db 1141 GATTGAGGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AGCGACAGCTGTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1260
1201 AGCGACAGCTGTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 AGCGACAGCTGTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAACAGATCATCAAAACTGCTGCTTCTCAAGTCAAGACTGGAATAATCAAAAGCATC 1320
1261 AAACAGATCATCAAAACTGCTGCTTCTCAAGTCAAGACTGGAATAATCAAAAGCATC 1320

Db	1361	AAAGAGATCATCAAAACATGCTGCGTCTCTGAAGTCAGAACTGGAAAAACATCAAAAACATC	1320
Qy	1321	TTTGTTTTTTGGGAATCCCCAAATTGTGCACTATTGCTCTGGGATCCCGTGATTTTGGACATC	1380
Db	1321	TTTTTTTTTGGGTGATCCCAATTTTGCAGTTTATTTCTCTGGGGATCCAAAGATTTTGTGACATTT	1380
Qy	1381	TACGACATATCAAACTGATGACTAGTCATGAAGGGGTGGAACTGTAACCAAGTTGTCAAGTCCCA	1440
Db	1381	TACGACATATCTAATATGATGTCTGCTATAGGGGTGGAAATTTTAACTACCTGTCAAGTCCCA	1440
Qy	1441	CCCAATATTCATTTCTGCAATCACAATTACTACAGCCCGGAAAGAGATGATTAACAATTC	1500
Db	1441	AGAAGCAATTCATTTCTGCATTAAGTCTAGTACATCTGCGAAGCAGATGGCATTCAGATTC	1500
Qy	1501	CTAAGAGACATTTGAGAACTGTGCAATCAATTCATGAAAGATTCCTAAAGCAACACACCA	1560
Db	1501	CTAAAGGATATCCGGGAAATCAGTCAACAACAAATTCATGAAGATTCCTAAAGCTTAACACCA	1560
Qy	1561	GGAAATGGGTGGCAATCTATATGCCATGGCCAGACCAACTGTGACAGAAATATGTTGGACAGA	1620
Db	1561	GGAAATGGGTGGCAATCTATATGCGATGTGGCCAGGCAACCATGACAGAAAGCTGTGGACAGA	1620
Qy	1621	TTGTCTCTAGTCTTCTTTGGACAGCTTGATACGACACGACACTGTACCCAGGAGCCAG	1680
Db	1621	ATATTCCTCCGCTCTTTGGACACTGCTTTATCTACGACACCCGCTGACTCAGGCAACACAG	1680
Qy	1681	ATGAATGGTTCTCGAAAACCCCATGTA	1707
Db	1681	ATGAACGGTTCTCCAAAAGCCCCGCTGA	1707

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RESULT 7
US-09-356-643B-5
: Sequence 5, Application US/09356643B
: Patent No. 656966
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
: TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR
: FILE REFERENCE: 200116.402C1
: CURRENT APPLICATION NUMBER: US/09/356,643B
: CURRENT FILING DATE: 1999-07-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 1707
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1707)
: US-09-356-643B-5

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Query Match	74.9%	Score 1278.2	DB 4	Length 1707
Best Local Similarity	84.3%	Pred. NO. 0		
Matches 1439	Conservative 0	Mismatches 268	Indels 0	Gaps 0

QY	1	ATGCGTCGACAGACCTTCCTGATGTTGAAGCCCTTGGACCCCTTAAAGATTTTGGAA	60
Db	1	ATGCGCGGAACCGACCTCTCTCAAGCTGAAGACCTTCGACCTTTTGGAGATTTTGGAA	60
QY	61	GTAATACCTCCAAAAAGCCAAAGATTTATGTAATAAGCATTTGCACACAGTATGAGCCCTGG	120
Db	61	TCTATTATCCACAAAAGGCCAAAGAAATTTATGTGATGATGAAATTGCAACCAATAATGAGCCCTGG	120
QY	121	CAGCTAATTGCGATGGAGTGTCTGTGAGAACCTCTGTATAGTCTTGGGATATGATTTGTC	180
Db	121	CAGCTCAATTCGCGGAGAGTGTCTGTGACCTCTGCTGATAGCTGTGGGTATGAGACCTTATC	180
QY	181	TTTCAGGCAGAGATTTATGTCAGAGTTTAAAAAGAAATGTTTAAAGCTCACACGAGAG	240
Db	181	TTTCAGGCACAGATTTATGTCGTCCGTTTAAAAAAATTTATTTAAGCTTATCAGAGAG	240

QY	241	ATGCCATTATTTGGACGCTAAGATCGAACACAGGTGAGCCAAAGAGATCTTGTGC	300
Db	241	ATGCCATTATTTGGACGCTAAGATCGAACACAGGTGAGCCAAAGAGATCTTGTGC	300
QY	301	AAGAACATGTCATTCTGAAAGTGACAAAGAGTATGTGAAAGCTTTACCTCCAGGGT	360
Db	301	AAGAACATGTCATTCTGAAAGTGACAAAGAGTATGTGAAAGCTTTACCTCCAGGGT	360
QY	361	CTGAGCTATCTGGCTGTTTGGAGAACTTTAAGSGTACAGTCTCATGAGAGCCCTTGG	420
Db	361	CTGAGCTATCTGGCTGTTTGGAGAACTTTAAGSGTACAGTCTCATGAGAGCCCTTGG	420
QY	421	CAAGAGGGGAGAGCCTCTGAAACAGTGTACAGTGGGGAGAGAAAGCTCACTGAGCTCTT	480
Db	421	CAAGAGGGGAGAGCCTCTGAAACAGTGTGTACATGGGGAGAACGAGCTCACGAGAGCTGCTG	480
QY	481	GTGAAGGTTTATGGAATTTTTCATAGGAGTAAACCCCTGCATCCAGATATCTTCCACAGA	540
Db	481	GTGACAGGTTTATGGAATTTTTCACGCGGAGCAATCCACGTGCATCCAGATATCTTCCCTGGA	540
QY	541	CTACGCAAGATAGAGAGCGAAATTTGTAGAGTACGTTTCTCCCTTTCATATGGGGAGACA	600
Db	541	TTGGGGAAAGTTAGAGCGCAAAATGCTTAGATGACTTGTCTCTCTTCAATGGGGAGACA	600
QY	601	GATTCTGTGATGTGTACTTTCTGGGGGAAACAGAACATATCTATGAGCTGCAACACA	660
Db	601	GATTCTGTGATGTGTACTTTCTGGGGGAAACGGAACATCTGTAGTGGCTGTCCAAAGCT	660
QY	661	TGTGGGGATCTGGCCTTTGAGAAAGGGGATCAAACTCCAGAAATTTGGGCTCCCAAGT	720
Db	661	TACCGGGACTTGGCGTTAGAGAGAGGGATCAAAACTCCAGAAATTTGTGGCTCCGAGAGT	720
QY	721	GCCCATGCTGCATTTTAAACAAAGCAGCCAGTTACTTTGGGATGAAGATTTGGCGGCTCCA	780
Db	721	GCCCATGCTGCATTTGACAAAGCAGCTATTATTTTGGGATGAAGATTTGCCAGATTTGCA	780
QY	781	TTGACGAAAGATAGTAGAGAGTGGATGTGAGGCAANTGAAAGCATCTCCAGAAAGCT	840
Db	781	CTGAAAAAGAACTAGAGAGTGGATGTGAGGCAANTGAAAGAGGCAATCTCCAGGAACACA	840
QY	841	GCCATGCTGCATTTTACCCACAGTTCCTCATGCTGAATAGATCTGTCCCTTAA	900
Db	841	GCTATGCTGCATTTGTATCCACACAGTTTCTCATGCTGAATAGATCTGTCCCGAA	900
QY	901	GTGGCCAAAGCTGGCTGTAAATACAAATACCCTTCACTGTTCGACGCTTGTCTGGGAGGC	960
Db	901	GTGGCCAAAGTTAACTGTGCTGATATAAAATCCACATCTGTGGAGTGTCTGGGGGGC	960
QY	961	TTTCTCATCTCTTATGAGAAAGCAGATACCCACGTGAGAGCACCATTGTGATTTCCGG	1020
Db	961	TTTCTCATCTCTTATGAGAAAGCAGAGTACCACGTGAGAGAAACATTTGATTTCCGG	1020
QY	1021	GTGAAGGTGTACCAAGCATTTTCAGAGATACATATAAGTATGGCTATGCTCTTAAAGT	1080
Db	1021	GTGAAGGTGTACCAAGCATTTTCAGAGATACATATAAGTATGGCTATGCTCTTAAAGT	1080
QY	1081	TCAATCATTTGGTGTATAGTACGAAAGTACAGAGACTTCAGATTTCTTGGTATGCA	1140
Db	1081	TCAATCATTTGGTGTATAGTACGAAAGTACAGAGACTTCAGATTTCTTGGTGTGCA	1140
QY	1141	GATTGGCAGAGGTGCATCTATGCTTTCCCAACATCGCAGGCTCAGGCGCTGTGGGCATTT	1200
Db	1141	GACTGGCAGAGGTGTGCTTACGCATCTCMAAGCATAGCTGGCTCAGGCGCTGTGGGCATTC	1200
QY	1201	AGCCGAGCCTGTGGGCTGCTTGAATGACATTCGCTGAGAAAGGCTATGTTGAAGCTTAC	1260
Db	1201	ATTGCACACCTGTTGGGGGCGCTTATGATGCACTTTCGGTGAAGACGCTATGTTGAAGCTTAC	1260
QY	1261	AAACAGATCATCAAAACATGCTGCTCTCTCAAGTACAGAACTGAGAAATATCAAAAGGATCTC	1320
Db	1261	AAACAGATCATCAAAACATGCTGCTCTCTCAAGTACAGAACTGAGAAATATCAAAAGGATCTC	1320

QY 1321 TTTGTTTGGGAATCCCAATGTCATCTGAGATCCCGTATTTGACATC 1380
 11 1111 11 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1321 TTGATTTTGGGATCCCAATGTCATCTGAGATCCCGTATTTGACATC 1380
 QY 1381 TACCGATCTCAATGTCATCTGAGATCCCGTATTTGACATC 1440
 1111 1111 11 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1381 TACCGATCTCAATGTCATCTGAGATCCCGTATTTGACATC 1440
 QY 1441 CCAGATTCATTTGTCATCTGAGATCCCGTATTTGACATC 1500
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 Db 1441 AGAAGATTCATTTGTCATCTGAGATCCCGTATTTGACATC 1500
 QY 1501 CTAAAGGATTCGAGATCTGTCATCTGAGATCCCGTATTTGACATC 1560
 1111 1111 11 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1501 CTAAAGGATTCGAGATCTGTCATCTGAGATCCCGTATTTGACATC 1560
 QY 1561 GGAATGGTGCATCTGATCTGAGATCCCGTATTTGACATC 1620
 1111 1111 11 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1561 GGAATGGTGCATCTGATCTGAGATCCCGTATTTGACATC 1620
 QY 1621 TTGCTCAGTCTTCTGAGATCCCGTATTTGACATC 1680
 1111 1111 11 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1621 ATATCTCGTCTTCTGAGATCCCGTATTTGACATC 1680
 QY 1681 ATGAATGTTCTTCAAAACCCCACTGA 1707
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1681 ATGAAGGTTCTTCAAAACCCCACTGA 1707

RESULT 8 US-08-939-309-9

Sequence 9, Application US/08939309
 Patent No. 6423527

GENERAL INFORMATION:

APPLICANT: Sada, Julie D.
 APPLICANT: Zhou, Jianhui
 TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 NUMBER OF INVENTION: METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED AND BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/939,309
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: David, Mark J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 200116,402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1467 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: Linear

FEATURE:

NAME/KEY: CDS
 LOCATION: 1..1464

US-08-939-309-9

Query Match 71.3%; Score 1217; DB 4; Length 1467;
 Best Local Similarity 85.9%; Pred. No. 0;
 Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1;

QY 1 ATGCTAGACAGACCTTCTGATTTGAAGGCTTTGAGCCCTTACCTTGAAGATTTGGAA 60
 1 ATGCTAGACAGACCTTCTGATTTGAAGGCTTTGAGCCCTTACCTTGAAGATTTGGAA 60
 Db 1 ATGCTAGACAGACCTTCTGATTTGAAGGCTTTGAGCCCTTACCTTGAAGATTTGGAA 60
 QY 61 GTATCTCCCAAAAGCCAAAGATTTATGTAATGACATTGACCAAGTATGAGCCCTGG 120
 61 GTATCTCCCAAAAGCCAAAGATTTATGTAATGACATTGACCAAGTATGAGCCCTGG 120
 Db 61 GTATCTCCCAAAAGCCAAAGATTTATGTAATGACATTGACCAAGTATGAGCCCTGG 120
 QY 121 CAGCTAATTCAGAGAGTGTGCTGAGAGCCCTGCTGATCTGAGGATTTGAGTTTGTG 180
 121 CAGCTAATTCAGAGAGTGTGCTGAGAGCCCTGCTGATCTGAGGATTTGAGTTTGTG 180
 Db 121 CAGCTAATTCAGAGAGTGTGCTGAGAGCCCTGCTGATCTGAGGATTTGAGTTTGTG 180
 QY 181 TTCCAGCAGAGAGTTTATGTCAGAGTTTAAAGAAATGTTTAAAGTCCACAGAGAG 240
 181 TTCCAGCAGAGAGTTTATGTCAGAGTTTAAAGAAATGTTTAAAGTCCACAGAGAG 240
 Db 181 TTCCAGCAGAGAGTTTATGTCAGAGTTTAAAGAAATGTTTAAAGTCCACAGAGAG 240
 QY 241 ATGCCATTTATTTGCTGTAAGATTCAAGACAGTTGACCAAGCAAGAGTATTTAGC 300
 241 ATGCCATTTATTTGCTGTAAGATTCAAGACAGTTGACCAAGCAAGAGTATTTAGC 300
 Db 241 ATGCCATTTATTTGCTGTAAGATTCAAGACAGTTGACCAAGCAAGAGTATTTAGC 300
 QY 301 AAGACATGTCATCTCGAAAGTGGACAAAGATGATGTAAGCTTTACCTCCAGAGGT 360
 301 AAGACATGTCATCTCGAAAGTGGACAAAGATGATGTAAGCTTTACCTCCAGAGGT 360
 Db 301 AAGACATGTCATCTCGAAAGTGGACAAAGATGATGTAAGCTTTACCTCCAGAGGT 360
 QY 361 CTGAGCTCATCTGCTTTTGGAGAAACTTAAGAGTACAGCTTATGAGAGCCCTTCTGG 420
 361 CTGAGCTCATCTGCTTTTGGAGAAACTTAAGAGTACAGCTTATGAGAGCCCTTCTGG 420
 Db 361 CTGAGCTCATCTGCTTTTGGAGAAACTTAAGAGTACAGCTTATGAGAGCCCTTCTGG 420
 QY 421 CAAGAGGGAGAGCCCTTGGACAGAGTGTACAGTGGGAGAGAGCAAGCTGAGCTCTT 480
 421 CAAGAGGGAGAGCCCTTGGACAGAGTGTACAGTGGGAGAGAGCAAGCTGAGCTCTT 480
 Db 421 CAAGAGGGAGAGCCCTTGGACAGAGTGTACAGTGGGAGAGAGCAAGCTGAGCTCTT 480
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 481 GTGAAGGCTATGAGAGTTTGGATGAGTACAGTACCCCTGATCAGATTTCTCCAGGA 540
 Db 481 GTGAAGGCTATGAGAGTTTGGATGAGTACAGTACCCCTGATCAGATTTCTCCAGGA 540
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 541 CTAGCGAATAGAGGAGAGAAATTTGAGAGTACCTTCTCCCTGTTCAATGGGGAGCA 600
 Db 541 CTAGCGAATAGAGGAGAGAAATTTGAGAGTACCTTCTCCCTGTTCAATGGGGAGCA 600
 QY 601 GATTCTGTGAGATGTGACTTCTGGGGAGACAGAAAGCATCTATGAGCTTGCAGAA 660
 601 GATTCTGTGAGATGTGACTTCTGGGGAGACAGAAAGCATCTATGAGCTTGCAGAA 660
 Db 601 GATTCTGTGAGATGTGACTTCTGGGGAGACAGAAAGCATCTATGAGCTTGCAGAA 660
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 661 TGTGCGGATCTGCTTTGAGAGGGGATCAAAATTCAGAAATTTGGCTCCCAAGT 720
 Db 661 TGTGCGGATCTGCTTTGAGAGGGGATCAAAATTCAGAAATTTGGCTCCCAAGT 720
 QY 721 GCCCATGCTGATTTAAAGAGAGCCAGTTTCTGAGTGAAGATTTGGCGGTCCTCA 780
 721 GCCCATGCTGATTTAAAGAGAGCCAGTTTCTGAGTGAAGATTTGGCGGTCCTCA 780
 Db 721 GCCCATGCTGATTTAAAGAGAGCCAGTTTCTGAGTGAAGATTTGGCGGTCCTCA 780
 QY 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGAGAGCTATCTCAGAGAAC 840
 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGAGAGCTATCTCAGAGAAC 840
 Db 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGAGAGCTATCTCAGAGAAC 840
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 Db 841 GCCATGCTGCTGTTTACCCACAGTTTCTGATGATGATTAATGATCTTCCAGAA 900
 QY 901 GTGCGCAAGCTGCTGTAATCAAAATACCCCTTATGATGATGATGATGATGATGAT 960
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 Db 901 GTGCGCAAGCTGCTGTAATCAAAATACCCCTTATGATGATGATGATGATGATGATGAT 960
 QY 961 TTCTCATGCTTTTATGAGAAAGCATATCCCACTGAGAGCAACCATTTGATTCGG 1020
 961 TTCTCATGCTTTTATGAGAAAGCATATCCCACTGAGAGCAACCATTTGATTCGG 1020
 Db 961 TTCTCATGCTTTTATGAGAAAGCATATCCCACTGAGAGCAACCATTTGATTCGG 1020


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OY 1021 GTGAAGGTGTACCAGCATTTACGCTGACACCCATAAGTATGCTATGCCCCAAAAGGC 1080
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OY 1081 TCATCATTTGGTGTATAGTACAGAAAGTACAGAACTATCATTTCTGTGATAC 1140
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DB 1060 ----- 1059
OY 1141 GATTGGCAGGGTGCATCTATGCTTCCCAACATCGACGCTCAGGCTGTGTGCATTC 1200
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DB 1060 ----- 1059
OY 1201 AGCCGAGCTGTGGGCTGCCCTTGATGACATTCGGTGAGAACGGCTATGTTGAACCTACC 1260
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DB 1060 ----- 1059
OY 1261 AACAGATCATCAAAACTGCTGCTTCCCAAGTACAGAACTGGAATAATATCAAGGCATTC 1320
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DB 1060 -----CTGGAATAATATCAAGGCATTC 1080
OY 1321 TTTGTTTTTGGGAATCCCAATTTGTCACTCATTTGCTGTGGATCCCGTATTTTGACATC 1380
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DB 1081 TTTGTTTTTGGGAATCCCAATTTGTCACTCATTTGCTGTGGATCCCGTATTTTGACATC 1140
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OY 1381 TACGACATATCAAACTATGATGCTGTAGGGGTGGAACCTTGAACCACTTGACAGTTCCCA 1440
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DB 1441 TACGACATATCAAACTATGATGCTGTAGGGGTGGAACCTTGAACCACTTGACAGTTCCCA 1200
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OY 1501 CTAAAGACATTCGAGAACTGTCACTCAATCATGAAGAAATCTTAAAGCGAAGACACA 1560
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DB 1261 CTAAAGACATTCGAGAACTGTCACTCAATCATGAAGAAATCTTAAAGCGAAGACACA 1320
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DB 1321 GGATGGGTGCATCTATGCTATGCGCCGACAGCACTGTGTGACAGAAATGTTGTCACAAA 1380
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OY 1621 TTGTCCTGAGTCTTCTTGACAGCTTGTACAGACGACATGTCACCCAGGCGAGCAG 1680
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DB 1381 TTGTCCTGAGTCTTCTTGACAGCTTGTACAGACGACATGTCACCCAGGCGAGCAG 1440
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OY 1681 ATGAATGGTCTCCAAAACCCCACTGA 1707
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DB 1441 ATGAATGGTCTCCAAAACCCCACTGA 1467

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RESULT 9

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US-09-849-180-9
; Sequence 9, Application US/09849180
; Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
            Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/849,180
; FILING DATE: 04-May-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pepe, Jeffrey C.
; REGISTRATION NUMBER: 46,985
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1464
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-849-180-9

Query Match      71.3%  Score 1217:  DB 4:  Length 1467:
Best Local Similarity 85.9%  Pred. No. 0:
Matches 1467:  Conservative  0:  Mismatches  0:  Indels  240:  Gaps  1:

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DB 1 ATGCTTACACAGACCTTCTGATGTTGAAGGCTTTGAGCCCTACTAGAGATTTTGGAA 60
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DB 61 GTATCTCCACAAAAGCCAGAAATATGTAATGACATTTGCACCACTATGAGCCCTGG 120
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DB 541 CTAGCAGATAGAGGAGAAATGTAGAGATAGCTTGTCCCTGTTCAATGGGGAGACA 600
OY 601 GATTGCTGTGATGTGACTTTCTGGGGAAACAGAAACATATCTATGCGCTTGCAGACA 660
DB 601 GATTGCTGTGATGTGACTTTCTGGGGAAACAGAAACATATCTATGCGCTTGCAGACA 660
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DB 661 TGTGGGAGATCGGCTTTGAGAGGGGATCAAACTCCAGAAATTTGTCCTCCCAAGT 720

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QY	781	TTGACGAAGATGATGAGAGTGGATGTGAGGGCAATGAGAAGAGCTATCTCAGAACT	840
Db	781	TTGACGAAGATGATGAGAGTGGATGTGAGGGCAATGAGAAGAGCTATCTCAGAACT	840
QY	841	GCCATGCTCGTCTGTCTTACCCACAGTTTCTCATGGTGTAAATAGATTCCTGTCCGAA	900
Db	841	GCCATGCTCGTCTGTCTTACCCACAGTTTCTCATGGTGTAAATAGATTCCTGTCCGAA	900
QY	901	GTGGCCAAAGCTGGGTGTCAAATACAAATACCCCTCATGTGCAGCGCTTCTCTGGAGGC	960
Db	901	GTGGCCAAAGCTGGGTGTCAAATACAAATACCCCTCATGTGCAGCGCTTCTCTGGAGGC	960
QY	961	TTCTCTATCGTCTTTATGAGAAAGCAGAGATACCCATGGAGACCCCATTTGATTCGG	1020
Db	961	TTCTCTATCGTCTTTATGAGAAAGCAGAGATACCCATGGAGACCCCATTTGATTCGG	1020
QY	1021	GTGAAGGTGTAAACAGCATTTTCAGCTGACACCCATTAAGTATGGCTTGGCCCCAAAGGC	1080
Db	1021	GTGAAGGTGTAAACAGCATTTTCAGCTGACACCCATTAAGTATGGCTTGGCCCCAAAGGC	1080
QY	1081	TCATCATTTGGTGTGTATGAGACAAAGATACGAATATCAGTCTTCTGTGATACA	1140
Db	1081	TCATCATTTGGTGTGTATGAGACAAAGATACGAATATCAGTCTTCTGTGATACA	1140
QY	1141	GATTGGCAGGGTGGCATCTATGCTTCCCAACCATTCGAGGCTCAGCGCTGTGGCATT	1200
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Db	1060	-----	1059
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Db	1081	TTTTTTTTTGGGAATCCCAATTTGTCACTCATTTGCTGTGGGATCCCGTGATTTTGACATC	1140
QY	1381	TACGACATCAAAACCTGATGACGTCTAAGGGGTGGAACCTTGAAACCACTTGACATTC	1440
Db	1141	TACGACATCAAAACCTGATGACGTCTAAGGGGTGGAACCTTGAAACCACTTGACATTC	1200
QY	1441	CCCAATTTTCTGTGATCACATTTACTACGCCCCGGAAACAGATAGCTATCAATTC	1500
Db	1201	CCCAATTTTCTGTGATCACATTTACTACGCCCCGGAAACAGATAGCTATCAATTC	1260
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QY	1561	GGAATGGGTGCATCTATGCCATGGCCAGACCACTGTGACAGAAATATGTTGCGAAA	1620
Db	1321	GGAATGGGTGCATCTATGCCATGGCCAGACCACTGTGACAGAAATATGTTGCGAAA	1380
QY	1621	TTGTCTCAAGTCTTCTTGGACAGTGTGTACAGCACGACATGTCACCCAGGAGCCAG	1680
Db	1381	TTGTCTCAAGTCTTCTTGGACAGTGTGTGTACAGCACGACATGTCACCCAGGAGCCAG	1440
QY	1681	ATGAATGGTCTTCCAAAACCCCACTGA	1707
Db	1441	ATGAATGGTCTTCCAAAACCCCACTGA	1467

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? Patent No.6569666
? GENERAL INFORMATION:
?
? APPLICANT: Saba, Julie D.
?
? TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
?
? TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
?
? TITLE OF INVENTION: METHODS OF USE THEREFOR
?
? FILE REFERENCE: 200116.40ZC1
?
? CURRENT APPLICATION NUMBER: US/09/356,643B
?
? CURRENT FILING DATE: 1999-07-19
?
? NUMBER OF SEQ ID NOS: 14
?
? SOFTWARE: FastSeq for Windows Version 4.0
?
? SEQ ID NO 9
?
? LENGTH: 1467
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? FEATURE:
?
? NAME/KEY: CDS
?
? LOCATION: (1)...(1467)
?
? US-09-356-643B-9

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Query Match	71.38; Score 1217; DB 4; Length 1467;
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Best local similarity: 0.78; Area: no: 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1;

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OY	61	GTATATCTCCACAAAAGCCACAGAAATTAATGTAATGGACATATGCAACCAAGTATGAGCCCTGG	120
Db	61	GTATATCTCCACAAAAGCCACAGAAATTAATGTAATGGACATATGCAACCAAGTATGAGCCCTGG	120
OY	121	CAGCTAATATGCATGGAGTGTGCTGTGGAGACCCGTGATGTGCTGGGGGATATGAGTTTGTG	180
Db	121	CAGCTAATATGCATGGAGTGTGCTGTGGAGACCCGTGATGTGCTGGGGGATATGAGTTTGTG	180
OY	181	TTTCCAGCCAGAGAGTTTATATGATCAAGGTTTAAAAAGAAATGTTTTAAGCTCACCAGGAAG	240
Db	181	TTTCCAGCCAGAGAGTTTATATGATCAAGGTTTAAAAAGAAATGTTTTAAGCTCACCAGGAAG	240
OY	241	ATGCCCATTTATTTGGTGTGTAAGATTTCAAGCAAGTGTACCAAGACCAAGATGATATTAGC	300
Db	241	ATGCCCATTTATTTGGTGTGTAAGATTTCAAGCAAGTGTACCAAGACCAAGATGATATTAGC	300
OY	301	AAGAACATGTCTTCTCCTGTAAGTGAACAAGAGTATGTAAAGCTTTACCCTTCCAGAGGT	360
Db	301	AAGAACATGTCTTCTCCTGTAAGTGAACAAGAGTATGTAAAGCTTTACCCTTCCAGAGGT	360
OY	361	CTGAGCTCATCTGCTGTTTGTGAGAACTTAAAGAGTACAGCTCTATGGAAGCTTCTGTG	420
Db	361	CTGAGCTCATCTGCTGTTTGTGAGAACTTAAAGAGTACAGCTCTATGGAAGCTTCTGTG	420
OY	421	CAAGAGGGAGAGCCCTGTGACAGTGTACAGTGGGGAGAGAAAGCTCACTGAGCTCTT	480
Db	421	CAAGAGGGAGAGCCCTGTGACAGTGTACAGTGGGGAGAGAAAGCTCACTGAGCTCTT	480
OY	481	GTGAAGGCTTATGAGAAATTTGCATGAGAGTAACCCCTGCATCCAGATATCTTCCAGGA	540
Db	481	GTGAAGGCTTATGAGAAATTTGCATGAGAGTAACCCCTGCATCCAGATATCTTCCAGGA	540
OY	541	CTAGCAGAGATGAGGCGACAAATTTGTGAGAGTAAGCTTGTCCCTGTTCATAGGGGGACCA	600
Db	541	CTAGCAGAGATGAGGCGACAAATTTGTGAGAGTAAGCTTGTCCCTGTTCATAGGGGGACCA	600
OY	601	GATTCGTGTGATGTGTGACTTCTGTGGGGACAGAAAGCATATCTCATGTGGCTCCAAAGCA	660
Db	601	GATTCGTGTGATGTGTGACTTCTGTGGGGACAGAAAGCATATCTCATGTGGCTCCAAAGCA	660
OY	661	TGTGGGAGATCTGGCTTTGAGAAAGGGAGTCAAAATCTCCAGAAATTTGGCTTCCCAAAAGT	720
Db	661	TGTGGGAGATCTGGCTTTGAGAAAGGGAGTCAAAATCTCCAGAAATTTGGCTTCCCAAAAGT	720
OY	721	GCCCATGTGTGATTTAACAAACAGCCAGCACTTACTTTGGGATGANAAGATTGTGCGGTCCCA	780

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Db      721 GCCCATGCTGCAATTTTAAAGAGGACGACATTTACTTTGGGATGTAAGATTGGCGGTCACA 780
QY      781 TTGACCAAGATGATGAGATGATGATGAGGCAATGAGAAGACATCTCTCCAGAACACT 840
Db      781 TTGACCAAGATGATGAGATGATGATGAGGCAATGAGAAGACATCTCTCCAGAACACT 840
QY      841 GCCATCTGCTGCTGCTTCTAAGCCCAAGTTTCTCATGCTGTAATAGATCTGCTCCGTA 900
Db      841 GCCATCTGCTGCTGCTTCTAAGCCCAAGTTTCTCATGCTGTAATAGATCTGCTCCGTA 900
QY      901 GTGGCCCAAGCTGGCTGTCAATTAATAATACCCCTTCATGCTGACGCTGTCTGGAGGC 960
Db      901 GTGGCCCAAGCTGGCTGTCAATTAATAATACCCCTTCATGCTGACGCTGTCTGGAGGC 960
QY      961 TTCCCTATGCTGCTTTATGAGAAAGCAGATACCACTGAGGACCCATTTGATTTCCGG 1020
Db      961 TTCCCTATGCTGCTTTATGAGAAAGCAGATACCACTGAGGACCCATTTGATTTCCGG 1020
QY      1021 GTGAAAGGTGTAAACGACATTTTCAGCTGACACCCCATAGTATGGCTATGCCCAAAAGGC 1080
Db      1021 GTGAAAGGTGTAAACGACATTTTCAGCTGACACCCCATAGTATGGCTATGCCCAAAAGGC 1080
QY      1081 TCATCATTTGGTGTGTATAGTACAAAGAACTACAGAACTATCATGTTCTTCGTGATACA 1140
Db      1081 TCATCATTTGGTGTGTATAGTACAAAGAACTACAGAACTATCATGTTCTTCGTGATACA 1140
QY      1141 GATTGGCAGGTTGGCATATGCTTCCCAACCATGGCAGGCTCAGGGCTGGTGCAATT 1200
Db      1141 GATTGGCAGGTTGGCATATGCTTCCCAACCATGGCAGGCTCAGGGCTGGTGCAATT 1200
QY      1201 AGCGAGCCTGTTGGGCTGCTTGATGACATTCGCTGAGAACGCGCTATGTGAAGCTACC 1260
Db      1201 AGCGAGCCTGTTGGGCTGCTTGATGACATTCGCTGAGAACGCGCTATGTGAAGCTACC 1260
QY      1261 AAACATATCATCAAACTGCTGCTTCTCAAGTCAAGTCAAACTGCAAAATATCAAAAGCATT 1320
Db      1261 AAACATATCATCAAACTGCTGCTTCTCAAGTCAAGTCAAACTGCAAAATATCAAAAGCATT 1320
QY      1321 TTTGTTTTGGGAATCCCAATTTGTCATCTGCTGAGATCCGCTGATTTTGACATC 1380
Db      1321 TTTGTTTTGGGAATCCCAATTTGTCATCTGCTGAGATCCGCTGATTTTGACATC 1380
QY      1381 TACCGATATCAAACTGATGACTGCTAAGGGGTGAACCTGAAACGATTTGCCA 1440
Db      1381 TACCGATATCAAACTGATGACTGCTAAGGGGTGAACCTGAAACGATTTGCCA 1440
QY      1441 CCCAGTATCTTTTGCATCTGACATTTACTACAGCCGCGGAAAGAGTACTATACATTTC 1500
Db      1441 CCCAGTATCTTTTGCATCTGACATTTACTACAGCCGCGGAAAGAGTACTATACATTTC 1500
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Db      1501 CTTAAAGACATTCGAGAACTCTGCTCAATCATGAAGATCTTAAAGGAAAGACACACA 1560
QY      1561 GGAATGGGTGCATCTATGCTGATGCGGCAAGAACTGTTGACAGAAATATGTTGAGAA 1620
Db      1561 GGAATGGGTGCATCTATGCTGATGCGGCAAGAACTGTTGACAGAAATATGTTGAGAA 1620
QY      1621 TTGTCTCAGCTGCTTGTGACAGCTTGTACAGACGACACTGTCAACCCAGGCGACGAG 1680
Db      1621 TTGTCTCAGCTGCTTGTGACAGCTTGTACAGACGACACTGTCAACCCAGGCGACGAG 1680
QY      1681 ATGAATGTTTTCGAAAACCCCACTGA 1707
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QY      1707 ATGAATGTTTTCGAAAACCCCACTGA 1707
Db      1707 ATGAATGTTTTCGAAAACCCCACTGA 1707

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RESULT 11
US-09-740-369-3
; Sequence 3, Application US/09740369
; Patent No. 6521437
; GENERAL INFORMATION:

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; APPLICANT: DUCKWORTH, DAVID MALCOLM
; APPLICANT: GODDEN, ROBERT JAMES
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30034-D1
; CURRENT APPLICATION NUMBER: US/09/740,369
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: EP 98300625.5
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: UK 9824026.0
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 09/238,373
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 785
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (129)(135)(147)(191)(193)(213)
US-09-740-369-3

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Query Match      16.7%; Score 284.4; DB 4; Length 785;
Best Local Similarity 97.2%; Pred. No. 6.5e-82;
Matches 307; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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QY      1394 ACCTGATGACTGCTAAGGGGTGGAAGTCAAGCAGTTGACGTTCCACCAATTTGATT 1453
Db      1 ACCTGATGACTGCTAAGGGGTGGAAGTCAAGCAGTTGACGTTCCACCAATTTGATT 60
QY      1454 TCTGATCATTACTACAGCGCCCGGAAGCAGTACTTAAATTTCTAAAGGACATTTC 1513
Db      61 TCTGATCATTACTACAGCGCCCGGAAGCAGTACTTAAATTTCTAAAGGACATTTC 120
QY      1514 GAGAACTCTGCACTCAATATCATGAAGAATCTTAAAGCAAGACACAGGAATGGTGCCA 1573
Db      121 GAGAACTCTGCACTCAATATCATGAAGAATCTTAAAGCAAGACACAGGAATGGTGCCA 180
QY      1574 TCTATGCCATGGCCGACGAACTGTGACAGAAATATGTTT-GCAGAAATTTG-CCATCAT 1631
Db      181 TCTATGCCATGGCCGACGAACTGTGACAGAAATATGTTTGGCAGAAATTTGCCCTCAGT 240
QY      1632 CTTCTTGACAGCTTGTACAGACGACAGCTGTACACCGAGGCGACAGATGATGATTTC 1691
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Db      301 TCCAAAACCCCACTGA 316

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RESULT 12
US-08-939-309-7
; Sequence 7, Application US/08939309
; Patent No. 6423527
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Mark J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
US-08-939-309-7

Query Match 15.0%; Score 256.2; DB 4; Length 1770;
Best Local Similarity 55.0%; Pred. No. 1,6e-72;
Matches 592; Conservative 0; Mismatches 473; Indels 12; Gaps 4;

QY 413 CCTCTGGCAAGAGGAGAGCCTTGGAACAGTGTACAGTGGGAGAGAGAGCTCATG 472
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QY 533 TCCAGAGCTACCAAGATAGAGAGCAAAATTTGAGATAGCTTGTCCCTGTCATG 592
DB 605 TTCTGCGCTACGTAATTAATGGAATCCGAATGTTTATGTTTAAAGATGTTATG 664
QY 593 GGGGACAGATTCGTGTGATGTGTG--ACTTCTGGGGAGAGAGAGCAATCTCATG 649
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QY 650 CCTGCAAGCATGTGGGATCTGGCTTTAGAA--GGGATCAAACTCCAGAAATTG 706
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QY 1004 ACCCATTTGATTTCCGGGTAAAGGTAAACGACATTTGACCTGACATACCATAGATG 1063
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QY 1064 GCTATGCCCCAAAGGCTCATCTGTTGTTATAGTGAACAAGATACAGAACTATC 1123
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DB 1325 GGTACATTTGAGTGTGCGCAAGATATGCTGCTGACAGATGATTAATAAATACATCC 1384
QY 1301 TGAATAATATCAAGGATCTTTGTTTGGAAATCCCAATTTGTCATGCTCTGG 1360
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RESULT 13
US-09-849-180-7
Sequence 7, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPINOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98035
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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DB 1330 GTTGAACTCTACAGATTCTCACTAAGTGAAGAAAAACATGTGCAACTGATGACTT 1389
OY 1432 CAGTCCGACCCAGATTATCTTCTGATCAGATTACTACACGCCCGGAAACGAGTACT 1491
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OY 1492 ATCAATTCTTAAGGACATTCGAGAACTCTGT 1523
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Search completed: October 6, 2003, 13:48:53
Job time : 119 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-053-510-7

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Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1707	100.0	1707	12	US-10-053-510-7
3	1707	100.0	1707	14	US-10-286-175-3
4	1702.2	99.7	1707	12	US-10-053-510-17
5	1699	99.5	2130	10	US-09-740-369-1
6	1699	99.5	5741	11	US-09-967-669-3
7	1278.2	74.9	1707	12	US-10-197-073-1
8	1278.2	74.9	1707	12	US-10-053-510-5
9	1278.2	74.9	1707	12	US-10-286-175-1
10	1217	71.3	1467	12	US-10-197-073-9
11	1217	71.3	1467	12	US-10-053-510-9
12	1217	71.3	1467	14	US-10-286-175-9
13	558	32.7	670	11	US-09-967-669-12
14	398.4	23.3	1658	12	US-10-053-510-15
15	364.8	21.4	474	11	US-09-967-669-11
16	284.4	16.7	785	10	US-09-740-369-3

17	256.2	15.0	1770	12	US-10-197-073-7	Sequence 7, Appl
18	256.2	15.0	1770	12	US-10-053-510-1	Sequence 1, Appl
19	256.2	15.0	1770	14	US-10-286-175-7	Sequence 7, Appl
20	241	14.1	54945	11	US-09-967-669-10	Sequence 10, Appl
21	225.6	13.2	1629	12	US-10-197-073-5	Sequence 5, Appl
22	225.6	13.2	1629	12	US-10-053-510-3	Sequence 3, Appl
23	225.6	13.2	1629	12	US-10-286-175-5	Sequence 5, Appl
24	80.2	4.7	3162	12	US-10-053-510-12	Sequence 12, Appl
25	68.4	4.0	243	9	US-09-923-876-202	Sequence 202, App
26	58.4	3.4	60	12	US-09-908-975-9862	Sequence 9862, Ap
27	38.6	2.3	1049	12	US-10-140-472-358	Sequence 358, App
28	38.6	2.3	1049	12	US-10-141-761-358	Sequence 358, App
29	38.6	2.3	1049	12	US-10-142-885-358	Sequence 358, App
30	38.6	2.3	1049	12	US-10-158-750-358	Sequence 358, App
31	38.6	2.3	1049	12	US-10-123-155-358	Sequence 358, App
32	38.6	2.3	1049	15	US-10-146-731-358	Sequence 358, App
33	38.2	2.2	802	14	US-10-184-644-312	Sequence 312, App
34	38.2	2.2	802	14	US-10-184-634-312	Sequence 312, App
35	37.8	2.2	3576	14	US-10-189-971-17	Sequence 17, Appl
36	37.8	2.2	3621	14	US-10-189-971-19	Sequence 19, Appl
37	37.8	2.2	4431	14	US-10-189-971-7	Sequence 7, Appl
38	37.8	2.2	4605	14	US-10-189-971-13	Sequence 13, Appl
39	37.8	2.2	4779	14	US-10-189-971-3	Sequence 3, Appl
40	37.6	2.2	1268	8	US-08-781-986A-293	Sequence 293, App
41	36.4	2.1	1056	13	US-10-027-633-30930	Sequence 30930, A
42	36.2	2.1	2277	14	US-10-189-971-21	Sequence 21, Appl
43	36.2	2.1	3173	14	US-10-189-971-5	Sequence 5, Appl
44	36.2	2.1	3753	14	US-10-189-971-15	Sequence 15, Appl
45	36.2	2.1	4026	14	US-10-189-971-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-197-073-3
Sequence 3, Application US/10197073
Publication No. US20030166897A1

GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197, 073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Uravter, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116, 40202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-10-197-073-3

Query Match 100.0%; Score 1707; DB 12; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ATGCTAGACAGACCTCTGATGTTGAAGCCCTTGAGCCCTACTTGAAGATTTGGAA 60
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121 CAGCTAATTTGATGAGAGTGTCTGTGACACCTGCTGATAGTCTGGGATATGATTTGTC 180
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901 GTGGCAAGCTGGCTGTAATAATACCCCTCATGTGAGAGCTGTGCTGGGAGGC 960
901 GTGGCAAGCTGGCTGTAATAATACCCCTCATGTGAGAGCTGTGCTGGGAGGC 960

901 GTGGCAAGCTGGCTGTAATAATACCCCTCATGTGAGAGCTGTGCTGGGAGGC 960
961 TTCTCATCTGCTCTTATGAGAGAAACAGAGATACCCACTGAGACACCATTTGATTTCCGG 1020
961 TTCTCATCTGCTCTTATGAGAGAAACAGAGATACCCACTGAGAGACCATTTGATTTCCGG 1020
1021 GTGAAGGCTGTAACAGCATTTTACCTGACAGACCCCTTAAGATGCTATGCCCCAAAGGC 1080
1021 GTGAAGGCTGTAACAGCATTTTACCTGACAGACCCCTTAAGATGCTATGCCCCAAAGGC 1080
1081 TCATCATTTGCTGTTATGATGACAAAGATGACAGAACTATCACTTCTGCTGATGACA 1140
1081 TCATCATTTGCTGTTATGATGACAAAGATGACAGAACTATCACTTCTGCTGATGACA 1140
1141 GATTGGCAGGGTGGCATCTATGCTTCCCAACATCGCAGGCTCAGGCTGCTGAGCAT 1200
1141 GATTGGCAGGGTGGCATCTATGCTTCCCAACATCGCAGGCTCAGGCTGCTGAGCAT 1200
1201 AGCGCAGCCTGTTGGGCTGCTTGTGATGACATTCGGTGAAGAGGCTATGTTGAAGCTACC 1260
1201 AGCGCAGCCTGTTGGGCTGCTTGTGATGACATTCGGTGAAGAGGCTATGTTGAAGCTACC 1260
1261 AAACAGATCATCAAAACAGCTGCTGCTTCCCAAGTGAAGAGTGAAGATATCAAAAGCATC 1320
1261 AAACAGATCATCAAAACAGCTGCTGCTTCCCAAGTGAAGAGTGAAGATATCAAAAGCATC 1320
1321 TTTGTTTTGGGAATCCCAATTTGCTACATCTGCTGAGATCCCTGATTTTGACATC 1380
1321 TTTGTTTTGGGAATCCCAATTTGCTACATCTGCTGAGATCCCTGATTTTGACATC 1380
1381 TACGACATCATCAAACTGATGATGCTTAAGGGGTGGAACCTTGAACCATTTGACATTTCCCA 1440
1381 TACGACATCATCAAACTGATGATGCTTAAGGGGTGGAACCTTGAACCATTTGACATTTCCCA 1440
1441 CCCGATTTATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1441 CCCGATTTATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1501 CTAAAGCAGATTCGAAATCTGTCACCTCAATCATGAAGATCTTAAAGCAGAGACACA 1560
1501 CTAAAGCAGATTCGAAATCTGTCACCTCAATCATGAAGATCTTAAAGCAGAGACACA 1560
1561 GGAATGGGTGGCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1561 GGAATGGGTGGCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1621 TTGCTCAGTCTTCTTGGAGACGTTGTACAGACGCTTGTACAGACGCTGTACAGACGCTGT 1680
1621 TTGCTCAGTCTTCTTGGAGACGTTGTACAGACGCTTGTACAGACGCTGTGTACAGACGCTGT 1680
1681 ATGAATGGTCTCCAAAACCCCACTGA 1707
1681 ATGAATGGTCTCCAAAACCCCACTGA 1707

RESULT 2
US-10-053-510-7
; Sequence 7, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Ryst, Henrik
; TITLE OF INVENTION: SPRINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.40ZC2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1707
; TYPE: DNA

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(1707)
 US-10-053-510-7

Query Match 100.0%; Score 1707; DB 12; Length 1707;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTTACGACACACCTTTGATGTGAAGCCCTTTAGACCCCTACTTAGAGATTTTGAA 60
DB 1 ATGCTTACGACACACCTTTGATGTGAAGCCCTTTAGACCCCTACTTAGAGATTTTGAA 60
QY 61 GTATCTCCACAAAAGCCCAAGATTTATGTAATGACATTGCACCAAGTATGACCCCTGG 120
DB 61 GTATCTCCACAAAAGCCCAAGATTTATGTAATGACATTGCACCAAGTATGACCCCTGG 120
QY 121 CAGCTAATTCATGAGTGTGCTGTGACCCCTGCTGATAGTGGGATATGAGTTTGTG 180
DB 121 CAGCTAATTCATGAGTGTGCTGTGACCCCTGCTGATAGTGGGATATGAGTTTGTG 180
QY 181 TTCCAGCCAGAGAGTTATGTGTCAGGTTTAAAAAGAAATGTTTAAAGCTCACCAGAG 240
DB 181 TTCCAGCCAGAGAGTTATGTGTCAGGTTTAAAAAGAAATGTTTAAAGCTCACCAGAG 240
QY 241 ATGCCCCATTTATGTCGTAAGATTCAGACAAAGTTGAACAAGACCAAGATGATTTAGC 300
DB 241 ATGCCCCATTTATGTCGTAAGATTCAGACAAAGTTGAACAAGACCAAGATGATTTAGC 300
QY 301 AAGAAATGTCATTCCTGAAAAGTGACAAAGATGATGAAAGCTTTACCCCTCCAGGGT 360
DB 301 AAGAAATGTCATTCCTGAAAAGTGACAAAGATGATGAAAGCTTTACCCCTCCAGGGT 360
QY 361 CTGAGCTCATCTGCTGTTTGGAGAAACTTAAGAGATGACAGCTATGAGACCTTCTGG 420
DB 361 CTGAGCTCATCTGCTGTTTGGAGAAACTTAAGAGATGACAGCTATGAGACCTTCTGG 420
QY 421 CAAGAGGGAGAGCCCTGGAACAGTGTACAGTGGGAGAGAGAGTCACTGAGCTCTT 480
DB 421 CAAGAGGGAGAGCCCTGGAACAGTGTACAGTGGGAGAGAGAGTCACTGAGCTCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCAATGCATATCTTCCAGGA 540
DB 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCAATGCATATCTTCCAGGA 540
QY 541 CTACGCAAGATAGAGCAAAATTTGACGATAGCTTTCCCTGTTCAATGGGAGACA 600
DB 541 CTACGCAAGATAGAGCAAAATTTGACGATAGCTTTCCCTGTTCAATGGGAGACA 600
QY 601 GATTGCTGTGGATGTGACTTCTGGGGGAACAGAAAGCATACATGAGCCCTGCAAGCA 660
DB 601 GATTGCTGTGGATGTGACTTCTGGGGGAACAGAAAGCATACATGAGCCCTGCAAGCA 660
QY 661 TGTGGGATCTGGCCTTTGAGAAAGGGGATCAAAATCTCAGAAATTTGTGCTCCCAAGT 720
DB 661 TGTGGGATCTGGCCTTTGAGAAAGGGGATCAAAATCTCAGAAATTTGTGCTCCCAAGT 720
QY 721 GGCATCTCTGATTTAAACAAAGCAGCTTACTTTGGGATGAAGATTTGTGGGTCCA 780
DB 721 GGCATCTCTGATTTAAACAAAGCAGCTTACTTTGGGATGAAGATTTGTGGGTCCA 780
QY 781 TTGACGAAGATGATGAGGTGATGATGAGGGCAATGAGAGATATCTCCAGAACACT 840
DB 781 TTGACGAAGATGATGAGGTGATGATGAGGGCAATGAGAGATATCTCCAGAACACT 840
QY 841 GCCATGCTCTGTTTACCCCAAGTTTCCATGATGATGATGATGATGATGATGATGAT 900
DB 841 GCCATGCTCTGTTTACCCCAAGTTTCCATGATGATGATGATGATGATGATGATGAT 900
QY 901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTATGTCAGAGCTTGTCTGGAGC 960
DB 901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTATGTCAGAGCTTGTCTGGAGC 960

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QY 961 TTCCATCTGCTTTTATGAGAAAGCAGATATCCACTGAGACACCCATTGATTTCCGG 1020
DB 961 TTCCATCTGCTTTTATGAGAAAGCAGATATCCACTGAGACACCCATTGATTTCCGG 1020
QY 1021 GTGAAGGTGTACACAGATTTTACGTCAGACACCCATTAAGTATGCTATGCCCAAGGC 1080
DB 1021 GTGAAGGTGTACACAGATTTTACGTCAGACACCCATTAAGTATGCTATGCCCAAGGC 1080
QY 1081 TCATCATTTGTTGTTATGATGACAAAGATGACAGAAATATCATGTTCTTCTGTGATACA 1140
DB 1081 TCATCATTTGTTGTTATGATGACAAAGATGACAGAAATATCATGTTCTTCTGTGATACA 1140
QY 1141 GATGCGAGGTGACATCTATGCTTCCCAACCATTCAGAGCTCAGGCTGAGGCTATT 1200
DB 1141 GATGCGAGGTGACATCTATGCTTCCCAACCATTCAGAGCTCAGGCTGAGGCTATT 1200
QY 1201 AGCGACCTGTGTGGCTGCTGTGATGACCTTCCGTTGAGAAAGGCTATGTTGAAGCTACC 1260
DB 1201 AGCGACCTGTGTGGCTGCTGTGATGACCTTCCGTTGAGAAAGGCTATGTTGAAGCTACC 1260
QY 1261 AATCAGATCATCAAAACTGCTCGCTTCCCTCAAGTCAGAACTGGAATAATCAAGGATC 1320
DB 1261 AATCAGATCATCAAAACTGCTCGCTTCCCTCAAGTCAGAACTGGAATAATCAAGGATC 1320
QY 1321 TTGCTTTTGGGAATCCCAATTTGTCACATCTGCTGAGATCCGCTGATTTGACATC 1380
DB 1321 TTGCTTTTGGGAATCCCAATTTGTCACATCTGCTGAGATCCGCTGATTTGACATC 1380
QY 1381 TACCGACTATCAAACTGATGACTGCTAAGGGGTGAACCTTGAACAGTTCACCTCCA 1440
DB 1381 TACCGACTATCAAACTGATGACTGCTAAGGGGTGAACCTTGAACAGTTCACCTCCA 1440
QY 1441 CCCAGTATTCATTTCTCATCTACATTAATCTACAGCCCGGAAGAGATATCAATTC 1500
DB 1441 CCCAGTATTCATTTCTCATCTACATTAATCTACAGCCCGGAAGAGATATCAATTC 1500
QY 1501 CTAAGGACATTCGAGATCTGTCTACATCAATCTGAAGATCTTAAGGCAAGACACA 1560
DB 1501 CTAAGGACATTCGAGATCTGTCTACATCAATCTGAAGATCTTAAGGCAAGACACA 1560
QY 1561 GGAATGGGTGCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 GGAATGGGTGCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 TTGCTCTAGCTCTTCTGAGACGTTGTACAGCACGACACTGTACCCAGGCGCAG 1680
DB 1621 TTGCTCTAGCTCTTCTGAGACGTTGTACAGCACGACACTGTACCCAGGCGCAG 1680
QY 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
DB 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707

```

RESULT 3
 US-10-286-175-3
 : Sequence 3, Application US/10286175
 : Publication No. US2003005922A1
 : GENERAL INFORMATION:
 : APPLICANT: Saba, Julie D.
 : Zhou, Jianhui
 : TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 : POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 : METHODS OF USE THEREFOR
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seed Intellectual Property Law Group
 : STREET: 701 Fifth Avenue, Suite 6300
 : City: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : ZIP: 98055
 : COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/286,175
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Steven J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200116,402C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-286-175-3

Query Match 100.0%; Score 1707; DB 14; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTAGACAGACCTCTGATGTTGAAGCCCTTGAGCCCTAGTAGAGATTTGGAA 60
DB 1 ATGCTAGACAGACCTCTGATGTTGAAGCCCTTGAGCCCTAGTAGAGATTTGGAA 60
QY 61 GATATCTCCAAAGCCAGAAATATGTAATGAGCATGACCAAGATATAGCCCTGG 120
DB 61 GATATCTCCAAAGCCAGAAATATGTAATGAGCATGACCAAGATATAGCCCTGG 120
QY 121 CAGCTAATTCATGAGAGTGTCTGTGAGACCTGCTGATAGTGTGGGATATGATTTGTC 180
DB 121 CAGCTAATTCATGAGAGTGTCTGTGAGACCTGCTGATAGTGTGGGATATGATTTGTC 180
QY 181 TTCACAGCCAGAGATTTATGTCAGAGTTTAAAAAGAAATGTTTAAGCTCACAGGAAG 240
DB 181 TTCACAGCCAGAGATTTATGTCAGAGTTTAAAAAGAAATGTTTAAGCTCACAGGAAG 240
QY 241 ATGCCCATATTTGGTGTGAAGTCAAGACAGTTGAACAGCAAGAGATATTTAGC 300
DB 241 ATGCCCATATTTGGTGTGAAGTCAAGACAGTTGAACAGCAAGAGATATTTAGC 300
QY 301 AAGAACATGTCATTCCTGAAAGTGAACAAAGATATGTGAAAGCTTTACCTCCAGGGT 360
DB 301 AAGAACATGTCATTCCTGAAAGTGAACAAAGATATGTGAAAGCTTTACCTCCAGGGT 360
QY 361 CTGAGCTATCTGCTGTTTGGAGAACTTAAAGAGTACAGCTCTATGAGACCTTTCTGG 420
DB 361 CTGAGCTATCTGCTGTTTGGAGAACTTAAAGAGTACAGCTCTATGAGACCTTTCTGG 420
QY 421 CAAGAGGGAGAGCCTGAGAGACGTATGACAGTGGGGAGAGAGACCTCACTAGCTCCTT 480
DB 421 CAAGAGGGAGAGCCTGAGAGACGTATGACAGTGGGGAGAGAGACCTCACTAGCTCCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGATCAGATATCTTCCAGGA 540
DB 481 GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGATCAGATATCTTCCAGGA 540
QY 541 CTACGCAAGATGAGGAGCAAAATTTGTAGAGATAGCTTGTCCCTGTTCAATGGGAGCA 600
DB 541 CTACGCAAGATGAGGAGCAAAATTTGTAGAGATAGCTTGTCCCTGTTCAATGGGAGCA 600
QY 601 GATTGCTGTGATGTACTCTCTGGGGAAACAGAAAGCATATGATGGCTGCAAGAGA 660
DB 601 GATTGCTGTGATGTACTCTCTGGGGAAACAGAAAGCATATGATGGCTGCAAGAGA 660

DB 601 GATTGCTGTGATGTACTCTCTGGGGAAACAGAAAGCATATGATGGCTGCAAGAGA 660
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DB 661 TGTGGGATGTGGCTTTGAGAGGGGATCAAAAGTTCAGAAATTTGTGGCTCCCAAGT 720
QY 721 GCCCATGCTGCATTTTAACAACAGCAGCACTTACTTTGGATGAAGATTTGGGGTCCCA 780
DB 721 GCCCATGCTGCATTTTAACAACAGCAGCACTTACTTTGGATGAAGATTTGGGGTCCCA 780
QY 781 TTGACGAAGATGATGAGGTGATGAGAGGGAATGAGAAAGCATATCTCCAGAACT 840
DB 781 TTGACGAAGATGATGAGGTGATGAGAGGGAATGAGAAAGCATATCTCCAGAACT 840
QY 841 GCCATGCTGCTGTGTTCTACCCCAAGTTCCTCATGTGTATAGATCTGTCCCTGAA 900
DB 841 GCCATGCTGCTGTGTTCTACCCCAAGTTCCTCATGTGTATAGATCTGTCCCTGAA 900
QY 901 GTGGCCAGCTGGCTGTCAAAATACAAATACCCCTTCATGTGAGAGCTTTGTGGAGGC 960
DB 901 GTGGCCAGCTGGCTGTCAAAATACAAATACCCCTTCATGTGAGAGCTTTGTGGAGGC 960
QY 961 TTCTCATGCTTTATGAGAGAGAGATACCCCACTGAGCAGCCATTGATTTCCGG 1020
DB 961 TTCTCATGCTTTATGAGAGAGAGATACCCCACTGAGCAGCCATTGATTTCCGG 1020
QY 1021 GTGAAAGGTATACAGCATTTTCAGCTGACACCCATATGATAGCTATGCCCAAAAGC 1080
DB 1021 GTGAAAGGTATACAGCATTTTCAGCTGACACCCATATGATAGCTATGCCCAAAAGC 1080
QY 1081 TCATCATTTGCTTTGTATATGTCAGAAAGTACAGAACTATCACTTCTCTCATATCA 1140
DB 1081 TCATCATTTGCTTTGTATATGTCAGAAAGTACAGAACTATCACTTCTCTCATATCA 1140
QY 1141 GATTGGCAGGGGTGATCATGCTTCCCAACCATGCAAGGCTCAGGGCTGTGGCATTT 1200
DB 1141 GATTGGCAGGGGTGATCATGCTTCCCAACCATGCAAGGCTCAGGGCTGTGGCATTT 1200
QY 1201 AGCGAGCCTGTTGGGCTGCTTATGATGACATTCGCTGAGAAAGGCTATGTTGAACCTAC 1260
DB 1201 AGCGAGCCTGTTGGGCTGCTTATGATGACATTCGCTGAGAAAGGCTATGTTGAACCTAC 1260
QY 1261 AAACAGATCATCAAAAGCTGCTGCTTCCCAAGTACAGAACTGGAATATCAAAAGCATC 1320
DB 1261 AAACAGATCATCAAAAGCTGCTGCTTCCCAAGTACAGAACTGGAATATCAAAAGCATC 1320
QY 1321 TTTGTTTTGGGAATCCCAATTTGACATTCATGCTCTGAGATCCCGTATTTTACATC 1380
DB 1321 TTTGTTTTGGGAATCCCAATTTGACATTCATGCTCTGAGATCCCGTATTTTACATC 1380
QY 1381 TACGACATATCAAAACCTGATGCTTAAGGGGTGAACCTTGAAACAGTTGCAATTCGA 1440
DB 1381 TACGACATATCAAAACCTGATGCTTAAGGGGTGAACCTTGAAACAGTTGCAATTCGA 1440
QY 1441 CCCATATTTATTTTCTGATCATGATTTACTACAGCCGCCGGAACGATATACAAATTC 1500
DB 1441 CCCATATTTATTTTCTGATCATGATTTACTACAGCCGCCGGAACGATATACAAATTC 1500
QY 1501 CCAAGTATTTCAATTTTGTGATCATGATTTACTACAGCCGCCGGAACGATATACAAATTC 1560
DB 1501 CCAAGTATTTCAATTTTGTGATCATGATTTACTACAGCCGCCGGAACGATATACAAATTC 1560
QY 1561 GGAATGGGTGCCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 GGAATGGGTGCCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 TTTGCTCAGTCTTTTGGAGAGCTTTGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1680
DB 1621 TTTGCTCAGTCTTTTGGAGAGCTTTGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1680
QY 1681 ATGAATGGTCTTCCAAACCCCACTGA 1707
DB 1681 ATGAATGGTCTTCCAAACCCCACTGA 1707

RESULT 4
US-10-053-510-17
; Sequence 17, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrist, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ. ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1707)
US-10-053-510-17

Query Match 99.7% Score 1702.2: DB 12: Length 1707:
Best Local Similarity 99.8% Pred. No. 0:
Matches 1704: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 1 ATGCGTAGCAGACGCTTCTGATGTGAGAGCCCTTTAGGCCCTTACTTAGAGATTTGGAA 60
Db 1 ATGCGTAGCAGACGCTTCTGATGTGAGAGCCCTTTAGGCCCTTACTTAGAGATTTGGAA 60
QY 61 GTATACTCCACAAAAGCCAAAGATTAATGTAATGACATTCGACCAAGATAGACCTCG 120
Db 61 GTATACTCCACAAAAGCCAAAGATTAATGTAATGACATTCGACCAAGATAGACCTCG 120
QY 121 CAGTATTCGATGAGTGTGTGAGAGCCCTGCTGATGATGCGGAGATATGATTTGTC 180
Db 121 CAGTATTCGATGAGTGTGTGAGAGCCCTGCTGATGATGCGGAGATATGATTTGTC 180
QY 181 TTCCAGCCAGAGAGTTTATGTCNAAGTTTAAAGAAATGTTTAAAGCTCACCAGAGAG 240
Db 181 TTCCAGCCAGAGAGTTTATGTCNAAGTTTAAAGAAATGTTTAAAGCTCACCAGAGAG 240
QY 241 ATGCCCCATTATGTCGTAAGATTCAAGACAGTTGAACAAGACCAAGATGATATTAGC 300
Db 241 ATGCCCCATTATGTCGTAAGATTCAAGACAGTTGAACAAGACCAAGATGATATTAGC 300
QY 301 AAGAACATGTCATTCCTGAAGAGTGACAAAGATGTAAGAGCTTACCCTCCAGAGT 360
Db 301 AAGAACATGTCATTCCTGAAGAGTGACAAAGATGTAAGAGCTTACCCTCCAGAGT 360
QY 361 CTGAGCTCATCTGCTGTTTTGAGAAACTTAAGAGAGTACAGCTTATGAGAGCCTTCG 420
Db 361 CTGAGCTCATCTGCTGTTTTGAGAAACTTAAGAGAGTACAGCTTATGAGAGCCTTCG 420
QY 421 CAAGAGGGAGAGCCTTGTGAACAGTGTACAGTGGGAGAGAAAGCTCAGCTCCTT 480
Db 421 CAAGAGGGAGAGCCTTGTGAACAGTGTACAGTGGGAGAGAAAGCTCAGCTCCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATCTTCCAGGA 540
Db 481 GTGAAGGCTTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATCTTCCAGGA 540
QY 541 CTACGCAAGATAGAGGCAAAATTTGAGAGTACCTTTCCCTGTTCAATGGGGAGCA 600
Db 541 CTACGCAAGATAGAGGCAAAATTTGAGAGTACCTTTCCCTGTTCAATGGGGAGCA 600
QY 601 GATTCTGTGATGTGTGACTTCTGGGGAGAACAGAAATCTCATAGGCGCTGCAAGCA 660
Db 601 GATTCTGTGATGTGTGACTTCTGGGGAGAACAGAAATCTCATAGGCGCTGCAAGCA 660

QY 661 TGTGGGATCTGCGCTTTTGAGAGGGGATCAAAATCTCCAGAAATTTGCTCCCAAGT 720
Db 661 TATCGGATCTGCGCTTTTGAGAGGGGATCAAAATCTCCAGAAATTTGCTCCCAAGT 720
QY 721 GCCCATCTGCAATTTAACAAAGCAGCAGTACTTTGGATGAAGATTTGCGGGTCCA 780
Db 721 GCCCATCTGCAATTTAACAAAGCAGCAGTACTTTGGATGAAGATTTGCGGGTCCA 780
QY 781 TTGACGAAGATGATGAGAGTGTGATGAGGCAATGAGAGACTATCTCCAGAACT 840
Db 781 TTGACGAAGATGATGAGAGTGTGATGAGGCAATGAGAGACTATCTCCAGAACT 840
QY 841 GCCATGCTCGCTTTTACCCACAGTTTCCATGATGTAATAGATCTGCTCCGAA 900
Db 841 GCCATGCTCGCTTTTACCCACAGTTTCCATGATGTAATAGATCTGCTCCGAA 900
QY 901 GTGGCAAGCTGCTGTCAAAATACAAATACCCCTTCATGTCAGCGCTGTGTGGAGGC 960
Db 901 GTGGCAAGCTGCTGTGTCAAAATACAAATACCCCTTCATGTCAGCGCTGTGTGGAGGC 960
QY 961 TTCTCATCGCTTTATGAGAGAAAGCAGATACCCACTGAGCACCATTTGATTTCCGG 1020
Db 961 TTCTCATCGCTTTATGAGAGAAAGCAGATACCCACTGAGCACCATTTGATTTCCGG 1020
QY 1021 GTGAAGGTGTAAACAGATTTTACGTCAGACCCCATTAAGTATGCTATGCCCCAAAGGC 1080
Db 1021 GTGAAGGTGTAAACAGATTTTACGTCAGACCCCATTAAGTATGCTATGCCCCAAAGGC 1080
QY 1081 TCATCATGTTGTGTATGATGACAAAGATGACGAACATATCAGTTCTTCTGCTGATACA 1140
Db 1081 TCATCATGTTGTGTATGATGACAAAGATGACGAACATATCAGTTCTTCTGCTGATACA 1140
QY 1141 GATTGGCAGGCTGCTATGCTTCCCAACATTCGAGGCTACAGGCTGTGTGGCATTT 1200
Db 1141 GATTGGCAGGCTGCTATGCTTCCCAACATTCGAGGCTACAGGCTGTGTGGCATTT 1200
QY 1201 AGGCGACCTGTTGGGCTGCTGATGACACTGCTGAGGAGAGGCTATGTTGAAGCTACC 1260
Db 1201 AGGCGACCTGTTGGGCTGCTGATGACACTGCTGAGGAGAGGCTATGTTGAAGCTACC 1260
QY 1261 AAGCAGATCATCAAAACTGCTGCTCTCAAGTCAGAACTGAGAAATATCAAAAGCATC 1320
Db 1261 AAGCAGATCATCAAAACTGCTGCTCTCAAGTCAGAACTGAGAAATATCAAAAGCATC 1320
QY 1321 TTTGTTTTTGGGAATCCCAATTTGTCACTATTCTCTGCGATCCCGATTTTGACATC 1380
Db 1321 TTTGTTTTTGGGAATCCCAATTTGTCACTATTCTCTGCGATCCCGATTTTGACATC 1380
QY 1381 TACGACATCAAACTGATGACTGTAAAGGGTGAAGACTGAACAGATTGACAGTCCCA 1440
Db 1381 TACGACATCAAACTGATGACTGTAAAGGGTGAAGACTGAACAGATTGACAGTCCCA 1440
QY 1441 CCCAGTATTCATTTCTGATCACAATTTACTACACCCCGGAAACAGATATGCAATTC 1500
Db 1441 CCCAGTATTCATTTCTGATCACAATTTACTACACCCCGGAAACAGATATGCAATTC 1500
QY 1501 CTAAAGGACATTCGAGAAATCTGTACTCAATATGAAAGATCTTAAAGGCAACACACA 1560
Db 1501 CTAAAGGACATTCGAGAAATCTGTACTCAATATGAAAGATCTTAAAGGCAACACACA 1560
QY 1561 GGAATGGGTGCACTATGACCTGAGGCGAGCACTGTTGACAGAAATATGTTGACAAA 1620
Db 1561 GGAATGGGTGCACTATGACCTGAGGCGAGCACTGTTGACAGAAATATGTTGACAAA 1620
QY 1621 TTGTCTCAGTCTTCTTGAGACGCTGTACAGCACGACACACTGTACCCAGAGGACGAG 1680
Db 1621 TTGTCTCAGTCTTCTTGAGACGCTGTACAGCACGACACACTGTACCCAGAGGACGAG 1680
QY 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
Db 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707

RESULT 6
US-09-967-669-3
; Sequence 3, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
; FILE REFERENCE: RFS-0259
; CURRENT APPLICATION NUMBER: US/09/967, 669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
; LENGTH: 5741
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-967-669-3

Query Match 99.58; Score 1699; DB 11; Length 5741;
Best Local Similarity 99.78; Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGCTAGCAGACCTCTGATGTTGAAGGCGCTTGGAGCCCTAGCTAGAGATTGGAA 60
DB 201 ATGCTAGCAGACCTCTGATGTTGAAGGCGCTTGGAGCCCTAGCTAGAGATTGGAA 260
QY 61 GATTAATCCACAAGGCAAGAAATTAATGATGACATGACCAAGATGAGCCCTGG 120
DB 261 GATTAATCCACAAGGCAAGAAATTAATGATGACATGACCAAGATGAGCCCTGG 320
QY 121 CAGCTAATGATGAGAGTGTGCTGAGCCCTCTGATAGTCTGGGATATGAGTTTGC 180
DB 321 CAGCTAATGATGAGAGTGTGCTGAGCCCTCTGATAGTCTGGGATATGAGTTTGC 380
QY 181 TTCACAGCAGAGAGTTTATGATGATTAAGAAATGTTTAAAGCTCACAGAGAG 240
DB 381 TTCACAGCAGAGAGTTTATGATGATTAAGAAATGTTTAAAGCTCACAGAGAG 440
QY 241 ATGCCCATTAATGCTGTAAGATTCAAGACAGTTGAACAAGCAAGATGATATTAGC 300
DB 441 ATGCCCATTAATGCTGTAAGATTCAAGACAGTTGAACAAGCAAGATGATATTAGC 500
QY 301 AAGAATGTCATCTCTGAAAGTGGACAAAGATATGTGAAGCTTTACCTCCAGGAT 360
DB 501 AAGAATGTCATCTCTGAAAGTGGACAAAGATATGTGAAGCTTTACCTCCAGGAT 560
QY 361 CTGAGCTCATCTCTGTTTGGAGAACTTAAGAGATACAGCTATGAGAGCCTTCTGG 420
DB 561 CTGAGCTCATCTCTGTTTGGAGAACTTAAGAGATACAGCTATGAGAGCCTTCTGG 620
QY 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAGCTCACTGAGCTCTT 480
DB 621 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAGCTCACTGAGCTCTT 680
QY 481 GTAAGGCTTATGGAATTTTGGATGAGTAAACCCCTGATCCAGATATCTTCCAGGA 540
DB 681 GTAAGGCTTATGGAATTTTGGATGAGTAAACCCCTGATCCAGATATCTTCCAGGA 740
QY 541 CTACGCAAGATAGAGCAGAAATTTGAGATAGCTTGTCCCTGTTCATATGGGGACCA 600
DB 741 CTACGCAAGATAGAGCAGAAATTTGAGATAGCTTGTCCCTGTTCATATGGGGACCA 800
QY 601 GATTGCTGTGATGTGTACTTCTGGGGAGAGAGAGCATCTCATGAGCTGCAAGCA 660
DB 801 GATTGCTGTGATGTGTACTTCTGGGGAGAGAGAGCATCTCATGAGCTGCAAGCA 860
QY 661 TGTGCGGATCTGCGCTTTGAGAGGGAGATCAAAATCTCCAAATTTGGCTCCCAAGT 720
DB 861 TGTGCGGATCTGCGCTTTGAGAGGGAGATCAAAATCTCCAAATTTGGCTCCCAAGT 920

QY 721 GCCCATCTGTCATTTAACAAGAGCAGCAGTACTTGGATGAAAGATTGTGGGGTCCCA 780
DB 921 GCCCATCTGTCATTTAACAAGAGCAGCAGTACTTGGATGAAAGATTGTGGGGTCCCA 980
QY 781 TTGACGAGATGATGAGGTGATGTGAGGGGCAATGAGAAAGACTATCTCCAGAACACT 840
DB 981 TTGACGAGATGATGAGGTGATGTGAGGGGCAATGAGAAAGACTATCTCCAGAACACT 1040
QY 841 GCCATCTGCTGCTGTTCTACCCCAAGTTTCCATGCTGCTATATGATCTGCTCCGAA 900
DB 1041 GCCATCTGCTGCTGTTCTACCCCAAGTTTCCATGCTGCTATATGATCTGCTCCGAA 1100
QY 901 GTGGCCAGCTGCTGCAATATCAAAATATCCCTTCATGCTGACGCTTGTGAGAGC 960
DB 1101 GTGGCCAGCTGCTGCAATATCAAAATATCCCTTCATGCTGACGCTTGTGAGAGC 1160
QY 961 TTCCCTCATGCTGTTTATGAGAAAGCAGATACCACCTGAGAGCACTTGAATTCGG 1020
DB 1161 TTCCCTCATGCTGTTTATGAGAAAGCAGATACCACCTGAGAGCACTTGAATTCGG 1220
QY 1021 GTGAAGGTGTAAACAGCATTTGACGTGACACCCATTAATATGCTATGGCCCAAGAGC 1080
DB 1221 GTGAAGGTGTAAACAGCATTTGACGTGACACCCATTAATATGCTATGGCCCAAGAGC 1280
QY 1081 TCATCATTTGCTGTTATAGTGAACAAGATACAGAACTATGATGCTTCTGCTGATACA 1140
DB 1281 TCATCATTTGCTGTTATAGTGAACAAGATACAGAACTATGATGCTTCTGCTGATACA 1340
QY 1141 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGCAAGGCTCACGGCTGTGGCAT 1200
DB 1341 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGCAAGGCTCACGGCTGTGGCAT 1400
QY 1201 AGGCGAGCCTGTTGGGCTGCTGATGACATTTGGGTGAGAAAGGCTATGTTGAAGCTACC 1260
DB 1401 AGGCGAGCCTGTTGGGCTGCTGATGACATTTGGGTGAGAAAGGCTATGTTGAAGCTACC 1460
QY 1261 AAACAGATCATCAAACTGCTGCTTCCCTCAATGACAACTGGAATAATCAAAAGGCTATC 1320
DB 1461 AAACAGATCATCAAACTGCTGCTTCCCTCAATGACAACTGGAATAATCAAAAGGCTATC 1520
QY 1321 TTTGTTTGGGAATCCCAATTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1521 TTTGTTTGGGAATCCCAATTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1580
QY 1381 TACCGACTATCAAACTGATGATGCTGTAAGGGGTGGAACCTTGAACCAAGTGGAGTCCCA 1440
DB 1581 TACCGACTATCAAACTGATGATGCTGTAAGGGGTGGAACCTTGAACCAAGTGGAGTCCCA 1640
QY 1441 CCCAGTATTCATTTCTGATACATTAATACAGCCCGGGAAGAGTATATACAAATTC 1500
DB 1641 CCCAGTATTCATTTCTGATACATTAATACAGCCCGGGAAGAGTATATACAAATTC 1700
QY 1501 CTAAAGGACATTTGAGAGATGCTGCTCAATCATGAGAAATCTTAAGGGAAGACCA 1560
DB 1701 CTAAAGGACATTTGAGAGATGCTGCTCAATCATGAGAAATCTTAAGGGAAGACCA 1760
QY 1561 GGAATGGGTGCAATCTATGCAAGGCGCCCAAGCAAGCTTGAAGGAATATGTTGCAAA 1620
DB 1761 GGAATGGGTGCAATCTATGCAAGGCGCCCAAGCAAGCTTGAAGGAATATGTTGCAAA 1820
QY 1621 TTGTCTCAGATCTTCTTGAACAGCTTGTACAGACCCAGCACTGTACACCCAGGAGCAG 1680
DB 1821 TTGTCTCAGATCTTCTTGAACAGCTTGTACAGACCCAGCACTGTACACCCAGGAGCAG 1880
QY 1681 ATGAATGCTTCTCCAAACCCCACTGA 1707
DB 1881 ATGAATGCTTCTCCAAACCCCACTGA 1907

RESULT 7
US-10-197-073-1
; Sequence 1, Application US/10197073
; Publication No. US2003016897A1

GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197,073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Drvater, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116,402D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-197-073-1
Query Match 74.98; Score 1278.2; DB 12; Length 1707;
Best Local Similarity 84.38; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;
QY 1 ATGCCCTGACAGAGCTTGTGATGATGAGGCTTTGAGCCCTAGTATGAGATTTTGAA 60
DB 1 ATGCCCGGAAACCGACCTCTCAAGCTGAGGACTTCGAGCTTATTGAGATTTTGAA 60
QY 61 GTATATCTCCAAAGGCAAGAAATTAATAATGAGATTCGACCAAGATATGAGCCCTG 120
DB 1 TCTTATTCACAAAGGCAAGAAATTAATAATGAGATTCGACCAAGATATGAGCCCTG 120
QY 121 CAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 CAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 TTCCAGCAGAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 TTCCAGCAGAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 ATGCCCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 ATGCCCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 AAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 AAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 CTGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 ATGGGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 421 CAAGAGGGAGAGCCCTGTGAAAGGTATGAGTGGGAGAGAGAGCTGAGCTCCTT 480
DB 421 CAAGAGGGAGAGCCCTGTGAAAGGTATGAGTGGGAGAGAGAGCTGAGCTCCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GTGAAGGCTTATGAGATTTTGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 CTACGAGATGAGAGGCAAGAAATTTGAGATGATGATGATGATGATGATGATGATGAT 600
DB 541 CTACGAGATGAGAGGCAAGAAATTTGAGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GATTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 GATTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 TGTGGGATCTGCGCTTTGAGAGAGGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 TGTGGGATCTGCGCTTTGAGAGAGGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 GCCCATGCTGATTTTAAACAAGCAGCCAGTACTTTGGAGATGAGATGATGATGATGAT 780
DB 721 GCCCATGCTGATTTTAAACAAGCAGCCAGTACTTTGGAGATGAGATGATGATGATGAT 780
QY 781 TTGACGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TTGACGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 GGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 GGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 GTGGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 GTGGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 TTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GTGAAGGCTTAAACAGAGATTTTCAAGCTGACACCCATAGTATGATGATGATGAT 1080
DB 1021 GTGAAGGCTTAAACAGAGATTTTCAAGCTGACACCCATAGTATGATGATGATGAT 1080
QY 1081 TCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 TCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GATTGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 GATTGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 AGCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 AGCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 AAACAGATCATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 AAACAGATCATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TTGCTTTTGGGAATCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TTGCTTTTGGGAATCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TACGAGATCATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TACGAGATCATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 CCCAGTATTCATTTCTGATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1500
DB 1441 AGAAGCATTCATTTCTGATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1500

Oy	1501	TTAAAGGCAATCGAGAACTGTGCATCAATCAATGAGAAATCCTAAAGCAACACACA	1560
Db	1301	CTAAAGGATATCCGGGAACTAGTACACAAATTCATGAAGAACTCTAAAGCTAAGACACA	1560
Oy	1561	GGAATGGGTGCATCTATATGCCATGGCCAGACCAACTGTTCACAGAAATATGTTGCAGAA	1620
Db	1561	GGAAATGGGTGCATCTATATGCCATGGCCAGACCAACTGTTCACAGAAATATGTTGCAGAA	1620
Oy	1621	TTGTCTCTCAGTCTTCTTTGGACAGCTTGTACAGCACCGACACTGTACCCAGGACGCAG	1680
Db	1621	ATATCTCTCCGCTTCTTCTTTGGACAGCTTGTATCTACGACCCCTGTGACTCAGAGGCACACAG	1680
Oy	1681	ATGAATGGTCTCTCCAAACCCCAACCTG	1707
Db	1681	ATGAACGGTCTCCCAAGCCCCCGCTGA	1707

```

RESULT 8
US-10-053-510-5
; Sequence 5, Application US/10053510
; Publication NO. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: Fyrlst, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1707)
US-10-053-510-5

```

Query Match	74.9%;	Score 1278.2;	DB 12;	Length 1707;
Best Local Similarity	84.3%;	Pred. No. 0;		
Matches 1439; Conservative	0;	Mismatches 268;	Indels 0;	Gaps 0;

OY	1	ATGCCCTACACAGACCTCTGTGATGTTGGAAGGCTTTGAGCCCTACTGTAGAGTTTGGAA	60
OY	1	ATGCCCGGAGACCGACCTCTCTCAAGCTGGAAGGACTTCGAGCCTTAATTGGACATTTTGGAA	60
Db	1	ATGCCCGGAGACCGACCTCTCTCAAGCTGGAAGGACTTCGAGCCTTAATTGGACATTTTGGAA	60
OY	61	GTATATCTCCACAAAAGCCAGAGATTTATGTAAATGACATTGCGACCAAGATATAGCCCTGG	120
Db	61	TCTTATTCACAAAAGCCAGAGATTTATGTGAATGATATTGCAACCAATATATAGCCCTGG	120
OY	121	CAGCTAATTGCGATGGAGTGTGCTGTGGACCCCTGCTGATATGCTGGGGATATGACATTTGTC	180
Db	121	CAGCTCAATTGGGTGGAGTGTCTCTGTACTCTGCTGATAGTCTGGGGTATATAGCCTTATTC	180
OY	181	TTCCGACGAGAGAGTTTATGGTCAGAGTTTTAAAGAAATGTTTAAAGCTCCACGGAAG	240
Db	181	TTCCGACGAGAGAGTTTATGGCTCTCGGTTTTAAAAAAATTTATTTAAAGTTTACGGAAG	240
OY	241	ATGCCCATTAATTGGCTGTACAGATTCCAAACACAGTTGAACACAGCAAGAGATATTTAGC	300
Db	241	ATGCCCATTTATTGGACGTATAGATCGAACACACAGGTGAGCAAGAACCAAGAGATCTTGTC	300
OY	301	AAGAACATGTCTATTTCTGTAAAGTGGACAAAAGTATGTGAAGCTTTAACTCTCCAGGGT	360
Db	301	AAGAACATGCCATTTCTTAAGGTGGACAAAGGATTTATGTGAAAAACCTGCTCTCAGGGT	360
OY	361	CTGACGCTATCTGCTGTTTTGGAGAAACTTAAAGAGATACGCTATATGAGCCCTTTGCG	420
Db	361	ATGGGACACAGCTGAGGTTCTGGAGAGACTCAAGAGAGTACAGCTTCATAGGATGGTTCTCGG	420

[illegible]

QY	1201	AGGCACCCCTGTTGGGCTGCCTTTGATGACATTCGGGTAGAAACGGCTATGTTGAAGCTATCC	1260
Db	1201	ATTGCACCCCTGTTGGGCGGCTTGTATGACACTTCGGGTAGAACGGCTATGTTGAAGCTATCC	1260
QY	1261	AAACAGATCATCAAAACGTGCTGGCTGCTCTCAAGTCAGAACATGTAAGAAATATATCAAAAGCATC	1320
Db	1261	AAACAGATCATCAAAACGTGCTGCTGCTCTCAAGTCAGAACATGTAAGAAATATATCAAAACATC	1320
QY	1321	TTTCTTTTGGGAATCCCAATATGTCATCTCATCTGCTGGATATCCGATTTTGACATC	1380
Db	1321	TTTCAATTTTCGGTGATTCCTCAATTTTCAAGTTATGTCCTGCGGATCAAAAGATTTTGACATTT	1380
QY	1381	TACCGACTATCAAAACCTGATGACACTCTAAGGGGTGAACTTGAACCAAGTTGCACTTCCCA	1440
Db	1381	TACCGACTATCTAATATGATGTCTGCTAAGGGGTGAATTTTAATCTACCTGCATGTTCCCA	1440
QY	1441	CCCGATTTCAATTTCTGATGACACATTTACTACTACGCCCGGGAAGAGATATAGCATATTC	1500
Db	1441	AGAGACATTAATTTCTGATTAATCTGATTAATCTGATTAATCTGGAAGCGAATGGCATCCAGTTC	1500
QY	1501	CTAAAGACATTTGAGAAATCTGTCACTCAATATCATGAAGAATCTCTAAAGCGAAGACCACA	1560
Db	1501	CTAAAGATATCCCGGAATCAGTCAACAAATCATGAAGAATCTCTAAAGCTAAGACCACA	1560
QY	1561	GGAAATGGGTGCATCTAATGCCATGCGCCACAGACACTGTGACACAGAAATATGTTGCGAGAA	1620
Db	1561	GGAAATGGGTGCATCTAATGGCATGCGCCACAGCAACATGACACAGAAAGCTGTGTCAGAA	1620
QY	1621	TTTGTCCTCAGATCTTCTTGAGACGCTGTACAGCACCAACTGTCAACCGACGGCAGCAG	1680
Db	1621	ATATCTCCGCGCTTCTTGAGACTGCTTTATATCTACGACCCCGCTGACTCAGAGGCAACACAG	1680
QY	1681	ATGAATGGTGTCTCCAAAACCCCACTGA	1707
Db	1681	ATGAACGGTGTCTCCAAAAGCCCGCTGA	1707

RESULT 10
 US-10-197-073-9
 ; Sequence 9, Application US/10197073
 ; Publication No. US20030166897A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saba, Julie D.
 ; Zhou, Jianhui
 ;
 ; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 ; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 ; METHODS OF USE THEREFOR
 ;
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed Intellectual Property Law Group
 ; STREET: 701 Fifth Avenue, Suite 6300
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98055
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/197, 073
 ; FILING DATE: 15-Jul-2002
 ; CLASSIFICATION: <unknown>
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Drvater, Julie A.
 ; REGISTRATION NUMBER: 50,461
 ; REFERENCE/DOCKET NUMBER: 200116.402D2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ;
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:

```

1      LENGTH: 1467 base pairs
2      TYPE: nucleic acid
3      STRANDEDNESS: single
4      TOPOLOGY: linear
5
6      FEATURE:
7          NAME/KEY: CDS
8          LOCATION: 1..1464
9      SEQUENCE DESCRIPTION: SEQ ID NO: 9
10     US-10-197-073-9

```

Query Match	71.3%;	Score 1217;	DB 12;	Length 1467;
Best Local Similarity	85.9%;	Pred. No. 0;		
Matches 1467;	Conservative	0;	Mismatches	0;
			Indels	240;
			Gaps	1;

QY	1	ATGCCCTACACAGACCTTGTAGTGTGAAGCCCTTGGAGCCCTACTCTGAGATTTTGGAA	60
Db	1	ATGCCCTACACAGACCTTGTAGTGTGAAGCCCTTGGAGCCCTACTCTGAGATTTTGGAA	60
QY	61	GTATACTCACAAAAGCCAAAGATTATGTAATGAGCATTTGCACCAACTATGAGCCCTGG	120
Db	61	GTATACTCACAAAAGCCAAAGATTATGTAATGAGCATTTGCACCAACTATGAGCCCTGG	120
QY	121	CAGCTAATTGCGATGGAGTGTGCTGTGAGACCCCTGCGATAGTCTGGGGATATGATGTTGTC	180
Db	121	CAGCTAATTGCGATGGAGTGTGCTGTGAGACCCCTGCGATAGTCTGGGGATATGATGTTGTC	180
QY	181	TTCCAGCCAGAGAGTTTATGCTCAAGGTTTTAAAAAGAAATGTTTTAAGCTCACAGGAAG	240
Db	181	TTCCAGCCAGAGAGTTTATGCTCAAGGTTTTAAAAAGAAATGTTTTAAGCTCACAGGAAG	240
QY	241	ATGCCCATTTATTTGGTCGTAAGATTCAACACAAGTTGAACAAGACCAGAAGATATTTAGC	300
Db	241	ATGCCCATTTATTTGGTCGTAAGATTCAACACAAGTTGAACAAGACCAGAAGATATTTAGC	300
QY	301	AAGAACATGTCATTCTCCGAAAGTGAGACAAAGAGTATGTAAAGCTTTACCCCTCCAGAGT	360
Db	301	AAGAACATGTCATTCTCCGAAAGTGAGACAAAGAGTATGTAAAGCTTTACCCCTCCAGAGT	360
QY	361	CTGAGCTCATCTGCTGTTTGGAGAACTTAAAGAGTACAGCTCTATGAGAGCCTTCTGG	420
Db	361	CTGAGCTCATCTGCTGTTTGGAGAACTTAAAGAGTACAGCTCTATGAGAGCCTTCTGG	420
QY	421	CAAGAGGGAGAGCCTCTGCAACAGTGTACAGTGGGAGAGAAAGCTCACTGAGCTCCTT	480
Db	421	CAAGAGGGAGAGCCTCTGCAACAGTGTACAGTGGGAGAGAAAGCTCACTGAGCTCCTT	480
QY	481	GTGAAGCTTATGAGATTTTTCATGAGATACCCCTGTCATCCAGATATCTTCCACAGA	540
Db	481	GTGAAGCTTATGAGATTTTTCATGAGATACCCCTGTCATCCAGATATCTTCCACAGA	540
QY	541	CTAGCAAGATATAGAGGCAAAATTTGTAGAGTACTTTCCTCGTTCAATGGGGAGACA	600
Db	541	CTAGCAAGATATAGAGGCAAAATTTGTAGAGTACTTTCCTCGTTCAATGGGGAGACA	600
QY	601	GATTGCTGTGATGTGTACTTCTGGGGGAGACAGAAAGCATACTCATGAGCCCTGCACAAACA	660
Db	601	GATTGCTGTGATGTGTACTTCTGGGGGAGACAGAAAGCATACTCATGAGCCCTGCACAAACA	660
QY	661	TGTGGGATCTGGCCTTTGAGAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
Db	661	TGTGGGATCTGGCCTTTGAGAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
QY	721	GCCCATGTGCAATTAAACAAAGACAGCCAGTTACTTTGGGATGAAATTTGGGGGTCCCA	780
Db	721	GCCCATGTGCAATTAAACAAAGACAGCCAGTTACTTTGGGATGAAATTTGGGGGTCCCA	780
QY	781	TTGACAGGAATGATGAGAGTGAATGTGAAGGCAATGAGAAGAAGCTATCTCCAGAAACT	840
Db	781	TTGACAGGAATGATGAGAGTGAATGTGAAGGCAATGAGAAGAAGCTATCTCCAGAAACT	840
QY	841	GCCATGCTGCTGCTGTTTCAACCCACAGTTTCTCATGCTGTAAATATGATCTCTCCCTGAA	900
Db	841	GCCATGCTGCTGCTGTTTCAACCCACAGTTTCTCATGCTGTAAATATGATCTCTCCCTGAA	900

QY 901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCATGTCAGCGCTTGTGGAGGC 960
|||||
Db 901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCATGTCAGCGCTTGTGGAGGC 960
QY 961 TTCCCTATGCTCTTTATGGAAGAGATACCCACTGAGACACCATTTGATTTCCGG 1020
|||||
Db 961 TTCCCTATGCTCTTTATGGAAGAGATACCCACTGAGACACCATTTGATTTCCGG 1020
QY 1021 GTGAAGGTGTAAACGACATTTGAGCTGACACCCATTAAGTATGCTATGCCCAAAAGC 1080
|||||
Db 1021 GTGAAGGTGTAAACGACATTTGAGCTGACACCCATTAAG----- 1059
QY 1081 TCATCATTTGGTGTGTATAGTGAACAAGATACAGAACTATCATGTTCTGTGATACA 1140
1060 ----- 1059
QY 1141 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGCGACGGCTGCTGGCATTT 1200
1060 ----- 1059
QY 1201 AGGCGAGCCTGTGGGCTGCTGATGCACTTGGGTGAGAGACGGCTATGTTGAAGCTACC 1260
1060 ----- 1059
QY 1261 AAACAGATCATCAAAACTGCTCGCTTCCTCAAGTCAAGACTGGAATAATATCAAGGCATC 1320
1060 -----CTGGAATAATATCAAAAGGCATC 1080
QY 1321 TTTGTTTTGGGAATCCCAATTTGTCATCTATGCTGTGGATCCGCTGATTTTGACATTC 1380
|||||
Db 1081 TTTGTTTTGGGAATCCCAATTTGTCATCTATGCTGTGGATCCGCTGATTTTGACATTC 1140
QY 1381 TACGCACTATCAAACTGATGACTGCTAAAGGGTGAAGTGAACCACTGACCTGCCA 1440
|||||
Db 1141 TACGCACTATCAAACTGATGACTGCTAAAGGGTGAAGTGAACCACTGACCTGCCA 1200
QY 1441 CCCGATATTCATTTTGCATCATCTACATGACAGCCCGGAAGAGTATATACAAATTC 1500
1201 CCCGATATTCATTTTGCATCATCTACATGACAGCCCGGAAGAGTATATACAAATTC 1260
QY 1501 CTAAAGACATTTGAGAGATTTGTCATCTCAATCATGAAGATCCTTAAGCGAAGACCACA 1560
|||||
Db 1261 CTAAAGACATTTGAGAGATTTGTCATCTCAATCATGAAGATCCTTAAGCGAAGACCACA 1320
QY 1561 GGAATGGGTGCATCTATGCGCATGGCCAGACAACTGTTGACAGGAATATGTTGCGAA 1620
1321 GGAATGGGTGCATCTATGCGCATGGCCAGACAACTGTTGACAGGAATATGTTGCGAA 1380
QY 1621 TTGTCTCATGCTTTCTTGACAGCTTTGACAGCAGCAGCACTGTCAACCCAGGCGAGCAG 1680
|||||
Db 1381 TTGTCTCATGCTTTCTTGACAGCTTTGACAGCAGCAGCACTGTCAACCCAGGCGAGCAG 1440
QY 1681 ATGAATGGTTCCTCAAAACCCCACTGA 1707
1441 ATGAATGGTTCCTCAAAACCCCACTGA 1467
Db

RESULT 12

US-10-286-175-9
; Sequence 9, Application US/10286175
; Publication No. US20030059922A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington

QY 1 COUNTRY: USA
; ZIP: 98055
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/286, 175
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Steven J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 200116, 402C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1464
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
; US-10-286-175-9:
Query Match 71.3%; Score 1217; DB 14; Length 1467;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1;
QY 1 ATCCCTAGACAGACCTCTGTGATGTTGAAGGCTTTGAGCCCTTACTAGAGATTTGGAA 60
Db 1 ATCCCTAGACAGACCTCTGTGATGTTGAAGGCTTTGAGCCCTTACTAGAGATTTGGAA 60
QY 61 GTATACCCCAAAAGCCAGAAATTAATGAAGACATGCAACCAAGTATGAGCCCTGG 120
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QY 121 CACCTAATTCATGAGAGTGTCTGTGAGACCCCTCTGATAGCTGGGATATGATTTGTC 180
Db 121 CACCTAATTCATGAGAGTGTCTGTGAGACCCCTCTGATAGCTGGGATATGATTTGTC 180
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Db 181 TTCCAGCCAGAGAGTTTATGTCAGAGTTTAAAGAAATGTTTAAAGTCACCGAGAG 240
QY 241 ATGCCCATTTTGTGCTGTAGATTTCAAGACAACTTGAACAAAGCAAGATGATATTAGC 300
Db 241 ATGCCCATTTTGTGCTGTAGATTTCAAGACAACTTGAACAAAGCAAGATGATATTAGC 300
QY 301 AAGAATGTCATCTTCTGAAAGTGAACAAAGATATGTAACCTTACCCAGAGGT 360
Db 301 AAGAATGTCATCTTCTGAAAGTGAACAAAGATATGTAACCTTACCCAGAGGT 360
QY 361 CTGAGCTCATCTGCTGTTTGGACAAACTTAAGAGTACAGCTATGAGCGCCTTCTGG 420
Db 361 CTGAGCTCATCTGCTGTTTGGACAAACTTAAGAGTACAGCTATGAGCGCCTTCTGG 420
QY 421 CAAGAGGGAGAGCCCTCTGGAACAGTACAGTGGGAGGAGGAAGCAAGCTCATGAGCTCTT 480
Db 421 CAAGAGGGAGAGCCCTCTGGAACAGTACAGTGGGAGGAGGAAGCAAGCTCATGAGCTCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGATCAGATATCTTCCAGGA 540
Db 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGATCAGATATCTTCCAGGA 540
QY 541 CTACGCAAGATAGAGCAGAAATTTGAGAGTATGCTTTCCTGTTCAATGGGGACCA 600
Db 541 CTACGCAAGATAGAGCAGAAATTTGAGAGTATGCTTTCCTGTTCAATGGGGACCA 600

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QY 601 GATTGCTGGATGTGTGACTTTGCGGGGAAACAGAAAGCAATCTATGGCTGCAAGCA 660
DB 601 GATTCGTGTGATGTGTGACTTCTGGGGGAAACAGAAAGCAATCTATGGCTGCAAGCA 660
QY 661 TGTGGGAAATCGGCTTTGAGAAAGGGAATCAAACTCCAGAAATGTGGCTCCCAAGT 720
DB 661 TGTGGGAAATCGGCTTTGAGAAAGGGAATCAAACTCCAGAAATGTGGCTCCCAAGT 720
QY 721 GCCCATGCTGCATTTACAAAGCAGCCAGTACTTTGGGATGAATGTGGCGGCTCCCA 780
DB 721 GCCCATGCTGCATTTACAAAGCAGCCAGTACTTTGGGATGAATGTGGCGGCTCCCA 780
QY 721 TTGACGAAGATGATGAGAGTGTGATGTGAGCGCAATGAGAAAGCTATCTCCAGAACT 840
DB 721 TTGACGAAGATGATGAGAGTGTGATGTGAGCGCAATGAGAAAGCTATCTCCAGAACT 840
QY 841 GCCATGCTGCTGCTGTCTACCCACAGTTCTCTATGGGATGATGATGATGATGATGAT 900
DB 841 GCCATGCTGCTGCTGTCTACCCACAGTTCTCTATGGGATGATGATGATGATGATGAT 900
QY 901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCAATGTCGAGCGTGTCTGGAGGC 960
DB 901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCAATGTCGAGCGTGTCTGGAGGC 960
QY 961 TTCCCTCATGCTTTTATGAGAAAGCAGATACCCACTGAGACACCCATTTGATTTCCGG 1020
DB 961 TTCCCTCATGCTTTTATGAGAAAGCAGATACCCACTGAGACACCCATTTGATTTCCGG 1020
QY 1021 GTGAAGAGGTATACAGCATTTTACGCTGACACCCCAATTAATGATGATGATGATGATGAT 1080
DB 1021 GTGAAGAGGTATACAGCATTTTACGCTGACACCCCAATTAATGATGATGATGATGATGAT 1080
QY 1081 TCATCATTTGATTTGTATAGTACAAAGATACAGAACTATCAGTTCTTCGTCATACA 1140
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QY 1141 GATTGGCAGGTTGGCATCTATGCTTCCCAACATCGAGGCTCAGGCTGTGGCATTT 1200
DB 1141 GATTGGCAGGTTGGCATCTATGCTTCCCAACATCGAGGCTCAGGCTGTGGCATTT 1200
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DB 1201 AGCGCAGCGCTGTGGGCTGCTGTATGACACTTCGCTGAGAAAGGCTATGTTGAAGCTACC 1260
QY 1261 AAACAGATCATCAAAATGCTGCTCTCTCAAGTCAGAACTGGAATAATCAAAAGCATC 1320
DB 1261 AAACAGATCATCAAAATGCTGCTCTCTCAAGTCAGAACTGGAATAATCAAAAGCATC 1320
QY 1321 TTTGTTTTTGGGAATCCCAATTTGCTACTCATTTGCTGTGGATCCCGTGATTTTGACATC 1380
DB 1321 TTTGTTTTTGGGAATCCCAATTTGCTACTCATTTGCTGTGGATCCCGTGATTTTGACATC 1380
QY 1381 TACGACATATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 TACGACATATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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QY 1561 GGAATGGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 GGAATGGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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DB 1621 TTTGCTCTAGTCTCTTGGAGAGCTTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1680
QY 1681 TTTGCTCTAGTCTCTTGGAGAGCTTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1740
DB 1681 TTTGCTCTAGTCTCTTGGAGAGCTTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1740
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QY 1681 ATGAATGGTCTCCAAACCCCACTGA 1707
DB 1441 ATGAATGGTCTCCAAACCCCACTGA 1467

RESULT 13
US-09-967-669-12
; Sequence 12, Application US/09967669
; Publication No. US2003092650A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
; FILE REFERENCE: R15-0259
; CURRENT APPLICATION NUMBER: US/09/967,669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 12
; LENGTH: 670
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-967-669-12
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Query Match 32.7%; Score 558; DB 11; Length 670;

Best Local Similarity 99.8%; Pred. No. 1,9e-175; Matches 569; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 47 TAGAGATTTTGGAAATATATCTCCACAAAGCCCAAGAAATATATGATGATGATGATGATGAT 106
DB 2 TAGAGATTTTGGAAATATATCTCCACAAAGCCCAAGAAATATATGATGATGATGATGATGAT 60
QY 107 AGTATGAGCCCTGGCAGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 166
DB 61 AGTATGAGCCCTGGCAGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 167 GATATGAGTTTGTCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 226
DB 121 GATATGAGTTTGTCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180
QY 227 AGCTCACCAGAAAGATGCCCATTTATGTCGTAAGATTCAGACAAAGTTGAACAGACCA 286
DB 181 AGCTCACCAGAAAGATGCCCATTTATGTCGTAAGATTCAGACAAAGTTGAACAGACCA 240
QY 287 AGGATGATATTTAGCAAGAAATGCTATTCCTGAAAGTGAGACAAAGATGATGATGATGATGAT 346
DB 241 AGGATGATATTTAGCAAGAAATGCTATTCCTGAAAGTGAGACAAAGATGATGATGATGATGAT 300
QY 347 TACCTCCCAAGGCTGTGAGCTCATCTGCTGTTTGGAAACTTAAAGATGATGATGATGATGAT 406
DB 301 TACCTCCCAAGGCTGTGAGCTCATCTGCTGTTTGGAAACTTAAAGATGATGATGATGATGAT 360
QY 407 TGGAGCGCTTCTGCGCAAGAGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGC 466
DB 361 TGGAGCGCTTCTGCGCAAGAGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGC 420
QY 467 TCATGAGCTCCTTGTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGATCCAG 526
DB 421 TCATGAGCTCCTTGTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGATCCAG 480
QY 527 ATATCTTCCAGAGATACGCAAGATGAGAGCGAAGAAATGTGAGATGATGATGATGATGATGAT 586
DB 481 ATATCTTCCAGAGATACGCAAGATGAGAGCGAAGAAATGTGAGATGATGATGATGATGATGAT 540
QY 587 TCAATGGGAGACAGATTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 646
DB 541 TCAATGGGAGACAGATTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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RESULT 14
US-10-053-510-15
; Sequence 15, Application US/10053510
; Publication No. US20030175939A1

Best Local Similarity 99.5%; Pred. No. 6,9e-111;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	1	GTGTAAGATTCAAGACAGTTGACACCAAGAGTATATTAGCAGACATGTCAT	60
OY	314	TCCTGAAGTGACAAAGAGTATGTGAAGCTTTACCCCTCCAGGGTCTGAGCTCATCTG	373
Db	61	TCCTGAAGTGACAAAGAGTATGTGAAGCTTTACCCCTCCAGGGTCTGAGCTCATCTG	120
OY	374	CTGTTTGGAGAACTTAAGAGTACACCTCTATGAGCGCCTTCTGGCAGAGGGAGAG	433
Db	121	CTGTTTGGAGAACTTAAGAGTACACCTCTATGAGCGCCTTCTGGCAGAGGGAGAG	180
OY	434	CCCTGGAACAGTGTACAGTGGGGAGAGAACTCACTGAGCTCCTTGTGAAGCTTATG	493
Db	181	CCCTGGAACAGTGTACAGTGGGGAGAGAACTCACTGAGCTCCTTGTGAAGCTTATG	240
OY	494	GAGATTTTGCATGGAGTAACCCCTGCATCCAGATATCTTCCAGGACTACGCAAGATAG	553
Db	241	GAGATTTTGCATGGAGTAACCCCTGCATCCAGATATCTTCCAGGACTACGCAAGATAG	300
OY	554	AGCAGAAATTGAGGATAGCTTGTCCCTGTTCAATGGGGAGACAGATTCTGTGAT	613
Db	301	AGCAGAAATTGAGGATAGCTTGTCCCTGTTCAATGGGGAGACAGATTCTGTGAT	360
OY	614	GTGTGACT 621	
Db	361	GTGTGACT 368	

Search completed: October 6, 2003, 13:46:51
Job time : 444 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2003, 09:57:10 ; Search time 3744 Seconds
(without alignments)
11081.127 Million cell updates/sec

Title: US-10-053-510-7
Perfect score: 1707
Sequence: 1 atgctagacacagactctt.....gtctccaaacccactga 1707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estbda:*
2: em_esthum:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estc:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1283	75.2	4006	AK037789 Mus muscu
2	1283	75.2	4008	AK043024 Mus muscu
3	1283	75.2	4009	AK036747 Mus muscu
4	1283	75.2	4030	AK049342 Mus muscu

5	1086.6	63.7	4361	11	AK030972	AK030972 Mus muscu
6	693	40.6	989	11	BX353997	BX353997 Mus muscu
7	671	39.3	3104	11	AK075851	AK075851 Mus muscu
8	639.4	37.5	1022	10	BB610497	BB610497 Mus muscu
9	619.8	36.3	976	13	BX353996	BX353996 Mus muscu
10	614.2	36.0	921	13	B0846030	B0846030 AGENCOURT
11	591.8	34.7	809	13	B0597239	B0597239 AGENCOURT
12	590.2	34.6	757	14	CD348713	CD348713 UI-M-FY0-
13	588.8	34.5	739	14	CA327176	CA327176 UI-M-FY0-
14	574.6	33.7	860	14	CB202317	CB202317 AGENCOURT
15	558	32.7	670	9	A1701419	A1701419 we29g09.x
16	551.6	32.3	734	14	CB247230	CB247230 UI-M-FY0-
17	542.8	31.8	666	10	BE467984	BE467984 h276g08.x
18	535.2	31.4	541	14	CA315356	CA315356 UI-M-FY0-
19	520.2	30.5	541	10	BF514352	BF514352 UI-M-FY0-
20	516.6	30.3	594	9	AL599962	AL599962 DKE2P31K
21	507.4	29.7	722	14	CB525257	CB525257 UI-M-FY0-
22	506.2	29.7	511	13	BX282607	BX282607 BX282607
23	503	29.5	843	13	BU166412	BU166412 AGENCOURT
24	490.2	28.7	772	14	CB249844	CB249844 UI-M-EX0-
25	486.4	28.5	746	13	B0442826	B0442826 UI-M-EX0-
26	482.8	28.3	801	10	BF787188	BF787188 602108947
27	482.6	28.3	766	12	BI103761	BI103761 602885462
28	480.2	28.1	800	14	CD348685	CD348685 UI-M-FY0-
29	475.2	27.8	963	10	BF310323	BF310323 601895151
30	472.6	27.7	632	13	B0769049	B0769049 UI-M-FC0-
31	472	27.7	655	12	BM963348	BM963348 UI-M-FC0-
32	470.2	27.5	979	13	B0714886	B0714886 AGENCOURT
33	468.8	27.3	614	9	AW822912	AW822912 UI-M-FY0-
34	458.4	26.9	614	9	BI105217	BI105217 602893494
35	451.4	26.4	705	12	BI105217	BI105217 602893494
36	449	26.3	457	9	AW651710	AW651710 ba62e01.y
37	448.8	26.3	541	12	BI047621	BI047621 MR4-SM024
38	445	26.1	545	10	BE504282	BE504282 h87f01.x
39	439.6	25.8	505	10	BE152613	BE152613 CM1-HT032
40	424.6	24.9	775	14	CB519417	CB519417 UI-M-GH0-
41	415.6	24.3	678	10	BF134806	BF134806 601779362
42	405.6	23.8	533	14	CD539780	CD539780 B0216C02-
43	403.8	23.7	533	13	BU249352	BU249352 603779780
44	402.4	23.6	728	10	BB612633	BB612633 Mus muscu
45	394.6	23.1	513	14	CD540179	CD540179 B0220D04-

ALIGNMENTS

RESULT 1
AK037789
LOCUS
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
cDNA clone: A130049P18 product: sphingosine phosphate lyase 1, full insert sequence.
ACCESSION AK037789
VERSION AK037789.1 GI:26332283
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
JOURNAL MEDLINE
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE
PUBMED
11042159

Dh 556 GTGACAGCTTATGAGAAATTCACGTGAGCAATTCACCTGCATCCAGATATCTTCCCTGGA 615
Qy 541 CTACGCAAGATAGAGCAGAAATTTGAGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
Dh 616 TTGCGGAAGTTAAGGACGAAATCGTTAGATGACTTGTCCCTTTCATGGGGAGCA 675
Qy 601 GATTGCTGTGATGTGTGACTTCTGGGGGAAAGAAACATCTCATGAGGCTGCAGAGCA 660
Dh 676 GATTCTGTGATGTGTGACTTCTGGGGGAAAGAAACATCTCATGAGGCTGCAGAGCT 735
Qy 661 TGTGCGGATCTGGCCTTTGAGAGGGGATCAAACTCCAGAAATTTGGCTCCCAAGT 720
Dh 736 TACCGGACTTGGCGTTAGAGAGGGGATCAAACTCCAGAAATTTGGCTCCCAAGT 795
Qy 721 GCCCATGCTCATTTAACAAGCAGCAGTTACTTGGGATGAGATTTGGCGGGTCCCA 780
Dh 796 GCCCATGCTCATTTAACAAGCAGCAGTTACTTGGGATGAGATTTGGCGGGTCCCA 855
Qy 781 TTGACGAGATGATGAGATGATGATGAGGCAATGAGAGAGCTATCTCCAGAGCACT 840
Dh 856 CTGAAAAGAAATGAGAGATGATGATGAGGCAATGAGAGAGCTATCTCCAGAGCACT 915
Qy 841 GCCATGCTGCTGCTTCTACCCACAGCTTCTCATGATGATGATGATGATGATGATGAT 900
Dh 916 GCTATGCTGCTGCTTCTACCCACAGCTTCTCATGATGATGATGATGATGATGATGAT 975
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Qy 1021 GTGAAAGCTTAACACAGCTTCTACCTGACACCCATAGATGATGATGATGATGATGAT 1080
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Qy 1081 TCATCATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Dh 1156 TCATCATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1215
Qy 1141 GATTGCGAGGCTGATCTATGCTTCCCAACATCCAGCTGAGCTGAGCTGAGCTGAGCT 1200
Dh 1216 GACTGGCAAGGCTGATCTATGCTGATCCAGAGCTGATGCTGATGCTGATGCTGATGCT 1275
Qy 1201 AGGCGACCTGTTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Dh 1276 ATTGCACCTGTTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1335
Qy 1261 AAACAGATCATCAAAATCTGCTGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1320
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Qy 1321 TTTGTTTTTGGGAATCCCAATTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Dh 1396 TTTGTTTTTGGGTATCTCAATTTGTCAATTTGTCTGCTGCTGCTGCTGCTGCTGCTG 1455
Qy 1381 TACCGATATCAAACTGATGATGCTGATGAGGGGATGAGCTTGAACCACTGCTGCTGCT 1440
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Qy 1441 CCCAGTATTCATTTCTGATCACAATTTCTACAGCCCGGAAAGAGATGATGATGATGAT 1500
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Qy 1501 CTAAGAGATTCGAGATGCTGCTCACTCAATCAATGAGAGATCCCTAAGGAGAGACCA 1560
Dh 1576 CTAAGAGATTCGAGATGCTGCTCACTCAATCAATGAGAGATCCCTAAGGAGAGACCA 1635
Qy 1561 GGAATGGCTGCTATGCTGATGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Dh 1636 GGAATGGCTGCTATGCTGATGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1695

Qy 1621 TTGTCCTAGCTTCTGTCAGACCTTGTACAGCAGCAGACTGTACACCGAGCCAG 1680
Dh 1696 ATATCCCTCCCTCTTCTTGAGCTGCTTATATACAGCAGCAGCCCTGATCAGGCGAC 1755
Qy 1681 ATGATGCTTCTCCAAACCCCACTGA 1707
Dh 1756 ATGACGCTTCTCCAAAGCCCGCTGA 1782
RESULT 2
AK043024
LOCUS
DEFINITION
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730048M17 product:sphingosine phosphate
lyase 1, full insert sequence.
ACCESSION
AK043024
VERSION
AK043024.1 GI:26335472
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakauechi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
REFERENCE
AUTHORS
Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Harada, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M.,
Quackenbush, J., Schmitt, L., Schmitt, L., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barish, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M., F. Brownstein, M., J. Bull, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D., A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazerrelli, J., Mommaerts, P., Nordone, P.,
Rising, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Tayo-Oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
and Hayashizaki, Y.
TITLE
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
MEDLINE
21085660

PUBMED 11217851
REFERENCES
AUTHORS
TITLE
JOURNAL
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.
Nature 420, 563-573 (2002)
(bases 1 to 4008)
Adechi, J., Alzawa, K., Akimura, T., Arekawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsumi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-Jul-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
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REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
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AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		

PUBMED
11042159

REFERENCE
AUTHORS

3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishii,K., Kitsuana,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakauechi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matukida,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
RIKEN Integrated sequence analysis (RISA) system -384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
11076861

TITLE

4 Kawai,J., Shitagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Araiawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Ozawa,M., Nishii,K., Kiyosawa,H., Kondo,S., Yamanaoka,I.,
Salto,T., Okazaki,Y., Gotohori,T., Bono,H., Kusunaga,T., Salto,R.,
Kadoya,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,M., Gaasterland,T., Gissi,C., King,B., Kochiba,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Peeble,G.,
Quackenbush,J., Schmitt,L.M., Staudt,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barish,G., Blake,J., Boftelli,D., Bojnaga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hall,D.,
Hotmann,M., Hume,D.A., Kamlay,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,T., Mombaerts,P., Nordone,P.,
Rilng,B., Rittwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Sessa,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Wiltaker,C., Wilmng,L.,
Wyshaw-Sorls,A., Yoshida,K., Hasegawa,Y., Kawai,H., Kotsukki,S.
and Hayashizaki,Y.

JOURNAL
MEDLINE
PUBMED
11217851

TITLE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4009)

JOURNAL
REFERENCE
AUTHORS

Adachi,J., Aizawa,K., Akinura,T., Araiawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hasegawa,K., Hatanaka,T., Hirozane,W.,
Hayashizaki,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Horii,F., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishii,K., Nomura,K., Numazaki,R., Ohno,M., Ohatao,N.,
Okazaki,Y., Salto,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physiological and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>,
Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>,
URL: <http://fantom.gsc.riken.go.jp/>.

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QY	1381	TACCGACATCAAAACCTGATGACCTTAAGGGGTGGAACCTTGAACCACTTGCAGTTC 1440
DB	1459	TACCGACATCAAAACCTGATGACCTTAAGGGGTGGAACCTTGAACCACTTGCAGTTC 1518
QY	1441	CCGAGTATTCATTTGTCATCATTATACAGCCCGGAAACGAGTACATATCAATTC 1500
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QY	1501	CTAAAGACATTCGAAATCTGTCTCACTCAATCATGAAGAAATCTTAAAGCAAGACACA 1560
DB	1579	CTAAAGACATTCGGAATCAGTACACAAATCATGAAGAAATCTTAAAGCTAAGACACACA 1638
QY	1561	GGAATGGTGCCATCTATAGCCATGGCCACAGACACTGTTGACAGGAATATGTTGTCAGAA 1620

Db 1639 GGATGCGTCCATCTATGCGATGCGCAGCAACATGACAGGAGCTGTTGCAGAA 1698
 Oy 1621 TTGGCCACGACTCTTCTGAGACGTTGTACAGCACCGACACTGTACACCGAGGAGCAG 1680
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 Db 1759 ATGACGCTTCTCCAAAGCCCGCTGA 1785

RESULT 4
 AK049342
 LOCUS
 DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone: C330025N24 product: sphingosine phosphatase lyase 1, full insert sequence.

ACCESSION AK049342
 VERSION AK049342.1 GI:26340063
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Carninci, P., and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420 563-573 (2002)
 REFERENCE 6 (bases 1 to 4030)
 AUTHORS Adachi, U., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 COMMENT Direct Submission
 TITLE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 URL: http://fantom.qualifiers

FEATURES
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 BASE COUNT
 ORIGIN

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	20499374 11042156	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunuma, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, K., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Takeda, Y., Ishikawa, T., Inoue, Y., Kira, A., and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome. Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	20530913 11076861	4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojodori, T., Bono, H., Kasukawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, M., Gaasterland, T., Glass, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldirelli, R., Barsch, G., Blake, J., Botfield, D., Bujunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, C., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ritzwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyono, O., Oka, K., Wang, K.H., Welter, C., Whitaker, C., Wilming, L., Wysshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	21083660 11217851	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	6 (bases 1 to 4361)	6 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Hayashida, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hukushida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, I., Hirozane, T., Horii, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koye, S., Kurihara, K., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/

OY	661	TGTCGGCATCGGCCTTTGAGAAAGGGATCAAACTCAGAAAATTGGCCGCCCAA	717
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LOCUS			
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ACCESSION	AK075851		
VERSION	AK075851.1	GI:26096560	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Carninci, P. and Hayashizaki, Y.		
AUTHORS	High-efficiency full-length cDNA cloning		
JOURNAL	Mech. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Irawa, M., Ohara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.		
RKEN	Integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer		
Genome Res.	10 (11), 1757-1771 (2000)		
JOURNAL	20530913		
PUBMED	11076661		
REFERENCE	4		
AUTHORS	Kawai, J., Shitagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaoka, I., Salto, T., Okazaki, Y., Gotohori, T., Bono, H., Kesukawa, T., Salto, R., Kodote, K., Matsuda, H., Ashburner, M., Batilov, S., Caaveant, T., Fleischmann, W., Gaasterland, T., Giusti, C., King, B., Kochiwa, H., Knehl, P., Lewis, S., Matsuo, Y., Nikolaic, I., Pesole, G., Quackenbush, J., Schiraldi, L.M., Stebbins, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Acno, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bolt, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Humé, D.A., Kamly, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Nordone, P., Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyok-Oka, K., Wang, K.H., Weitz, C., Wittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohzuki, S. and Hayashizaki, Y.		
FUNCTIONAL annotation of a full-length mouse cDNA collection	Nature 409 (6821), 685-690 (2001)		
JOURNAL	21085660		
MEDLINE	11217851		
PUBMED	5		
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		

TITLE	Analysis of the mouse transcriptome based on functional annotation									
JOURNAL	of 60,770 full-length cDNAs									
REFERENCE	Nature 420, 563-573 (2002)									
AUTHORS	b (bases 1 to 3104)									
	Aachti,J., Alzawa,K., Akinura,T., Arikawa,T., Bono,H., Carninci,P.,									
	Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,									
	Hayashida,K., Hayatsu,N., Hiramoto,K., Hiroka,T., Hirozane,T.,									
	Hori,F., Imomani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,									
	Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koude,M.,									
	Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,									
	Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,									
	Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,									
	Sano,H., Sasaki,D., Shibata,K., Shikagawa,A., Shiraki,T.,									
	Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,									
	Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,									
	Muraetsu,M. and Hayashizaki,Y.									
TITLE	Direct Submission									
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of									
	Physical and Chemical Research (RIKEN), Laboratory for Genome									
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),									
	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,									
	Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.go.jp,									
	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,									
	Fax:81-45-503-9216)									
COMMENT	cDNA library was prepared and sequenced in Mouse Genome									
	Encyclopedia Project of Genome Exploration Research Group in Riken									
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.									
	Division of Experimental Animal Research in Riken contributed to									
	prepare mouse tissues									
	Please visit our web site for further details.									
	URL:http://genome.gsc.riken.go.jp/									
	URL:http://fantom.gsc.riken.go.jp/.									
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 Db 301 TTGTTGTGTGAGCTGGCAGGGTGGTGTCTACCATCTCCAAAGCATAGCTGGCTCAGG 360
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 QY 1609 ATGTTGACAAATTCCTAAAGGATTCGAGATTCGAGATTCGAGATTCGAGATTCGAGATTC 1661
 Db 781 CTGTTGACAAATTCCTAAAGGATTCGAGATTCGAGATTCGAGATTCGAGATTCGAGATTC 833

RESULT 9
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 ACCESSION BX353996
 VERSION BX353996.1 GI:30371821
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 976)
 L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5671.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC013DE09NP1&cluster=5671.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/InvitrogenCorporation1600
 Faraday Avenue Genoscope sequence ID : CS0DC013DE09NP1.
 FEATURES
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT
 265 a 199 c 239 g 260 t 13 others
 ORIGIN
 Query Match 36.3%; Score 619.8; DB 13; Length 976;
 Best Local Similarity 98.1%; Pred. No. 2.4e-170;
 Matches 662; Conservative 6; Mismatches 3; Indels 4; Gaps 4;
 QY 1033 ACCAGCATTTAGCTGACACCCATTAAGTATGCTATGCCCCAAAGGCTCATTTGGTG 1092
 Db 971 ACCAGCATTTAGCTGACACCCATTAAGTATGCTATGCCCCAAAGGCTCATTTGGTG 914
 QY 1093 TTGATATGTGACAAGAGTACAGACATCATGTTCTTCGATACAGATTTGGCAGGGCT 1152
 Db 913 TTGATATGTGACAAGAGTACAGACATCATGTTCTTCGATACAGATTTGGCAGGGCT 856
 QY 1153 GGCATCTATGCTTCCCAACCATCGACGGCTCAGGGCTGCTGATGAGCCAGGAGCTGT 1212
 Db 855 GGCATCTATGCTTCCCAACCATCGACGGCTCAGGGCTGCTGATGAGCCAGGAGCTGT 796
 QY 1213 TTGGCTGCTTGTATGACACTTGGGTGAGAGCGCTATGTTGAAGCTACCAACAGATCATC 1272
 Db 795 TTGGCTGCTTGTATGACACTTGGGTGAGAGCGCTATGTTGAAGCTACCAACAGATCATC 736
 QY 1273 AAAAGTCTGCTTCCCAACCATCGACGGCTCAGGGCTGCTGATGAGCCAGGAGCTGT 1332
 Db 735 AAAAGTCTGCTTCCCAACCATCGACGGCTCAGGGCTGCTGATGAGCCAGGAGCTGT 676
 QY 1333 AATCCCAATTTGATCACTATTTGCTGGGATCCGCTGATTTTGAATCTTACCGACTATCA 1392
 Db 675 AATCCCAATTTGATCACTATTTGCTGGGATCCGCTGATTTTGAATCTTACCGACTATCA 616
 QY 1393 AACTGATGACTGCTAAGGGGTGGAAGTGAACAGTGTGACAGTGTCCACCAAGATTCAT 1452
 Db 615 AACTGATGACTGCTAAGGGGTGGAAGTGAACAGTGTGACAGTGTCCACCAAGATTCAT 556
 QY 1453 TTGTCATCACTACTACACAGCCCGGAAGACGAGTACGTATACAAATTCCTAAAGGACTT 1512
 Db 555 TTGTCATCACTACTACACAGCCCGGAAGACGAGTACGTATACAAATTCCTAAAGGACTT 496
 QY 1513 CGAAGATCTGTCACTCAATCATGAAGAAATCTTAAAGCGAAGACACAGAAATGGTGCC 1572
 Db 495 CGAAGATCTGTCACTCAATCATGAAGAAATCTTAAAGCGAAGACACAGAAATGGTGCC 436
 QY 1573 ATCTATGCTAGGCGCCAGACACACTGTGTGACAGAAATATGTTGAGAAATTTCTCTCAGTC 1632
 Db 435 ATCTATGCTAGGCGCCAGACACACTGTGTGACAGAAATATGTTGAGAAATTTCTCTCAGTC 376
 QY 1633 TTCTTGGACAGCTGTACAGACCGACAGCTGTCAACCGAGGACCGACAGATGAATGTTTCT 1692
 Db 375 TTCTTGGACAGCTGTACAGACCGACAGCTGTCAACCGAGGACCGACAGATGAATGTTTCT 316
 QY 1693 CCAAAACCCACTGA 1707
 Db 315 CCAAAACCCACTGA 301

RESULT 10
 B0846030 921 bp mRNA linear EST 16-OCT-2002
 LOCUS B0846030

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DEFINITION  AGENCOURT_10413219 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:5579973 5', mRNA sequence.
ACCESSION   BU846030
VERSION     BU846030.1 GI:24030735
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 921)
AUTHORS    NIH-MGC http://mhc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgsbbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Rublin Laboratory
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1CM2784 row: c column: 13
           High quality sequence stop: 640.
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         /db_xref="taxon:9606"
         /clone="IMAGE:6579973"
         /tissue_type="teratocarcinoma, cell line"
         /lab_host="DH10B (phage-resistant)"
         /clone_lib="NIH_MGC_109"
         /note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
         XhoI; cDNA made by oligo-dT priming. Directionally cloned
         into EcoRI/XhoI sites using the following 5' adaptor:
         GGCAAGAG(G). Library constructed by Ling Hong in the
         laboratory of Gerald M. Rubin (University of California,
         Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
         Superscript II RT (Life Technologies). Note: this is a
         NIH_MGC library."
BASE COUNT  240 a 186 c 294 g 200 t 1 others
ORIGIN
Query Match 36.0%; Score 614.2; DB 13; Length 921;
Best Local Similarity 94.3%; Pred. No. 1e-168;
Matches 660; Conservative 0; Mismatches 34; Indels 6; Gaps 2;
OY 1 ATGGCTACACAGACCTCTGATGTGTAAGCCCTTGAGCCCTACTTAGAGATTTTGGA 60
    |||||||
DB 206 ATGCTACACAGACCTCTGATGTGTAAGCCCTTGAGCCCTACTTAGAGATTTTGGA 265
OY 61 GTATACCTCCAAAAGCCAAAGATTAATGATGACATTCACCAATGATGAGCCCTGG 120
    |||||||
DB 266 GTATACCTCCAAAAGCCAAAGATTAATGATGACATTCACCAATGATGAGCCCTGG 325
OY 121 CAGCTAATTGATGAGAGTGTGCTGACCCCTGCTGATATGTCGGGATATGAGTTTGC 180
    |||||||
DB 326 CAGCTAATTGATGAGAGTGTGCTGACCCCTGCTGATATGTCGGGATATGAGTTTGC 385
OY 181 TTCACGACAGAGAGTTTGTGTCAGAGTTTAAAGAAATTTTAACTCACCACAGAG 240
    |||||||
DB 386 TTCACGACAGAGAGTTTGTGTCAGAGTTTAAAGAAATTTTAACTCACCACAGAG 445
OY 241 ATGCCCATTTATGTCGTAGATTCAGACAAAGTTGAACAAGACCAAGATGATATTAGC 300
    |||||||
DB 446 ATGCCCATTTATGTCGTAGATTCAGACAAAGTTGAACAAGACCAAGATGATATTAGC 505
OY 301 AAGAATATGTCATTCCTGGAAGAGTGAACAAGATGTAAGAGCTTTACCTCCAGGGT 360
    |||||||
DB 506 AAGAATATGTCATTCCTGGAAGAGTGAACAAGATGTAAGAGCTTTACCTCCAGGGT 565
OY 361 CTGAGCTATCTGCTGTTTGGAGAAACTTAAGAGATACACTATGAGACGCTTCTGG 420

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DB 566 CTGAGCTATCTGCTGTTTGGAGAACTTAAGAGATACAGCTCATGAGACGCTTCTGG 625
OY 421 CAAGAGGAGAGACCTCTGGAACAGTGTACAGTGGGAGAGAGACCTCAGCTCCCTT 480
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DB 626 CAAGAGGAGAGACCTCTGGAACAGTGTACAGTGGGAGAGAGACCTCAGCTCCCTT 685
OY 481 GTGAAGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAGATATCTTCCACGA 540
    |||||||
DB 686 GTGAAGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAGATATCTTCCACGA 745
OY 541 CTACCAAGATAGAGACGAGAAATTTGTAGAGATAGCTTGTCCCTTTCAATGGGGACCA 600
    |||||||
DB 746 CTACCAAGATAGAGACGAGAAATTTGTAGAGATAGCTTGTCCCTTTCAATGGNGAACA 805
OY 601 GATT----CGTGTGATGTGTCATCTTCGGGAGACAGAACATCACTATGAGCCCTGCA 656
    || |||
DB 806 GAATTCGGGTGATGATGTGTGACTTCTGTGGGGGAAACCGAAGCATATGATGCTGGCA 865
OY 657 AGCATGTGCGG--ATCTGGCCTTTGAGAAGGGGATCAAA 694
    || |||
DB 866 AACATATCGGGGATCTGGGCTTGAAGAGGGGATCAAA 905
RESULT 11
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LOCUS     AGENCOURT_8966006 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6454047
DEFINITION 5', mRNA sequence.
ACCESSION   B0597239
VERSION     B0597239.1 GI:23248998
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 809)
AUTHORS    NIH-MGC http://mhc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgsbbs-remail.nih.gov
           Tissue Procurement: NCI
           cDNA Library Preparation: Michael Brownstein Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1CM2630 row: h column: 16
           High quality sequence stop: 570.
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         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="IMAGE:6454047"
         /tissue_type="mixed (pool of 40 RNAs)"
         /lab_host="DH10B (T1-phage-resistant)"
         /clone_lib="NIH_MGC_142"
         /note="Vector: pDNR-LIB; Site_1: SfiI (ggccatctagcc);
         Site_2: SfiI (ggccgcctggcc); Double-stranded cDNA was
         prepared from a pool of 40 cell line polyA+ RNAs (bladder
         - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
         4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
         kidney - 2.2%, liver - 5.7%, lung - 10.4%, NK-cell - 5.2%,
         ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
         gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
         used in cloning as follows:
         5'-AAGCAGTGTATCAACGAGAGTGGCCATTAACGCGCGG-3' and
         5'-ATTCTAGAGCGGAGGCGGCGGACATG-dT(30)NN-3'. Full-length
         enriched library was constructed using the Clontech
         Creator SMART kit and size-selected to contain the >0.5 kb

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size fraction (other fractions present in NIH_MGC_141).
Library created in the Laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH MGC Library."

BASE COUNT

212 a 164 c 255 g 178 t

Query Match 34.7%; Score 591.8; DB 13; Length 809;
Best Local Similarity 97.9%; Pred. No. 3.6e-162;
Matches 610; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

1 ATGCTTACGACAGACCTTTGATGTGAAGCCCTTTGAGCCCTTACATAGAGATTTGGAA 60
186 ATGCTTACGACAGACCTTTGATGTGAAGCCCTTTGAGCCCTTACATAGAGATTTGGAA 245
61 GTATATCCACAAAGCCAAATTAATGATGACATTCACCAAGATATAGAGCCCGG 120
246 GTATATCCACAAAGCCAAATTAATGATGACATTCACCAAGATATAGAGCCCGG 305
121 CAGCTAATTCAGATGAGTGTGTCGACCCCTGCTGATAGTCTGGGATATAGATTTGTC 180
306 CAGCTAATTCAGATGAGTGTGTCGACCCCTGCTGATAGTCTGGGATATAGATTTGTC 365
181 TTCACGACAGAGATTTATGTCAGGTTTAAAAAGAAATTTTAACTTACACAGAGAG 240
366 TTCACGACAGAGATTTATGTCAGGTTTAAAAAGAAATTTTAACTTACACAGAGAG 425
241 ATGCCCATTTATTTGGTGTGAATTCAGACAAAGTTGAACCAAGACCAAGATATATAGC 300
426 ATGCCCATTTATTTGGTGTGAATTCAGACAAAGTTGAACCAAGACCAAGATATATAGC 485
301 AAGAATATGTCATTCCTGAAAGTGGACAAAGATATGTAAGGTTTAACTTACCCAGAGGT 360
486 AAGAATATGTCATTCCTGAAAGTGGACAAAGATATGTAAGGTTTAACTTACCCAGAGGT 545
361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATACACTCATATGAGAGCCCTTGG 420
546 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATACACTCATATGAGAGCCCTTGG 605
421 CAAGAGGAGAGAGCTCTGAAACAGTGTACAGTGGGAGGAGAGAGTCTAGTACCTCTT 480
606 CAAGAGGAGAGAGCTCTGAAACAGTGTACAGTGGGAGGAGAGAGTCTAGTACCTCTT 665
481 GTGAAGGCTTATGAGATTTTGCATGGAACCCCTGATCCAGATATCTTCCAGAGA 540
666 GTGAAGGCTTATGAGATTTTGCATGGAACCCCTGATCCAGATATCTTCCAGAGA 725
QY 541 CTACGCAAGATAGAGGCAAGAAATTTGAGATAGCTT-GTTCCTGTTCAATGGGGAGC 599
Db 726 CTACGCAAGATAGAGGCAAGAAATTTGAGATAGCTTGTCCCTGTTCAAGGGGGAGC 785
QY 600 AGATTGCTGTGATGTGACTT 622
Db 786 AATTCGGGTGATGGGGGCTT 808

RESULT 12
CD348713 757 bp mRNA linear EST 29-MAY-2003
LOCUS
DEFINITION
UT-M-FY0-cf8-1-11-0-UT.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6855348 5', mRNA sequence.
ACCESSION
CD348713
VERSION
CD348713.1 GI:31140228
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 757)
NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution Information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.

FEATURES
source
Location/Qualifiers

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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6855348"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpd"
/lab_host="DH10B (T1 phage resistant)"
/clone.lib="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hefin Chin, Ph.D.,
Program coordinator."

BASE COUNT 193 a 170 c 190 g 203 t 1 others

Query Match 34.6%; Score 590.2; DB 14; Length 757;
Best Local Similarity 86.4%; Pred. No. 1e-161;
Matches 652; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

685 GGGATCAAAATCTCCGAAATTTGTGGCTCCCAAGTGGCCATGTCATTTAAACAAACA 744
3 GGGATCAAAATCTCCGAAATTTGTGGCTCCCAAGTGGCCATGTCATTTAAACAAACA 62
QY 745 GCCAGTTACTTTGGAGTGAAGATTTGGGGTCCCATTTAGCAGAAATGAGGTGAT 804
Db 63 GCTCATTTATTTGGGATGAAGATTTGTCGAGTTGCACTGAAGAAACATGAGGTGAT 122
QY 805 GTGAGGCAATGAGAGAGCTATCTCCAGGAACATGCGCATGCTGTTGTTACCCCA 864
Db 123 GTGAGGCAATGAGAGAGCTATCTCCAGGAACATGCGCATGCTGTTGTTACCCCA 182
QY 865 CAGTTTCTCATGTTGATATGATTCCTGCTCCCTGAGGCAAGCTGGTCAAAATAC 924
Db 183 CAGTTTCTCATGTTGATATGATTCCTGCTCCCTGAGGCAAGCTGGTCAAAATAC 242
QY 925 AAATATCCCTTCATGTCGAGCTTTGTCGAGGAGCTTCTTCATGCTTTATGAGAAA 984
Db 243 AAATATCCCTTCATGTCGAGCTTTGTCGAGGAGCTTCTTCATGCTTTATGAGAAA 302
QY 985 GCAGGATATCCAGTGGAGACACCATTTATTTCCGGGTGAAAGGTGAACAGCATTTCA 1044
Db 303 GCAGGATATCCAGTGGAGACACCATTTATTTCCGGGTGAAAGGTGAACAGCATTTCA 362
QY 1045 GCTGACCCCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
Db 363 GCAGATATCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
QY 1105 AAGAATGACAGAACTATCACTTCTGTCATACAGATTTGCAAGGTGATGATGATCT 1164
Db 423 GAGAAGTACAGAGATCACTTCTGTCATACAGATTTGCAAGGTGATGATGATGATGAT 482

QY 1165 TCCCAACATGCGAGGCTCAGCGCTGCTGCTAGCGCAGCTGTTGGGCTGCTTG 1224
DB 483 TCCTCAAGATAGCTGCTCAGCGCTGCTGCTAGCTAGCTGCTGCTGCTGCTG 542
QY 1225 ATGCACCTGGGAGAGCGCTATGTTGAAGCTACCAACAGATCATCAAACTGCTGC 1284
DB 543 ATGCACCTGGGAGAGCGCTATGTTGAAGCTACCAACAGATCATCAAACTGCTGC 602
QY 1285 TTCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1344
DB 603 TTCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 662
QY 1345 TCACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
DB 663 TCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
QY 1405 GCTAAGGGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1439
DB 723 GCTAAGGGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 757

RESULT 13
CA327176 739 bp mRNA linear EST 27-NOV-2002
LOCUS
DEFINITION
UT-M-FV0-ccy-c-24-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6826033 5', mRNA sequence.
CA327176
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 739)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source
Seq primer: pyx-5
Location/Qualifiers
1..739
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6826033"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pyx-Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with Not I and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

Query Match 34.5%; Score 588.8; DB 14; Length 739;
Best Local Similarity 87.4%; Pred. No. 2,6e-161;
Matches 644; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
ORIGIN
BASP COUNT 183 a 168 c 201 g 186 t 1 others

575 CTTGTTCCCTGCTTCATATGGGGGACGAGTTCGTGGATGTGACTTCTGGGGAGACG 634
DB 3 CTTGTTCCCTGCTTCATATGGGGGACGAGTTCGTGGATGTGACTTCTGGGGAGACG 62
QY 635 AAAGCATCTCATATGCGCTCCAAAGCATGTCGGGATGCGCTTTGAAGGGAGTCAAA 694
DB 63 AAAGCATCTCATATGCGCTCCAAAGCATGTCGGGATGCGCTTTGAAGGGAGTCAAA 122
QY 695 CTCACAAATTTGGCTCCCAAGAGTCCCATGCTCATTTTAACAAAGCAGCCAGTTACT 754
DB 123 CTCACAAATTTGGCTCCCAAGAGTCCCATGCTCATTTTAACAAAGCAGCCAGTTACT 182
QY 755 TTGGGATGAAGATGTCGGGCTCCCATTCAGCAAGATGATGGAGTGTGAGGAGCA 814
DB 183 TTGGGATGAAGATGTCGGGCTCCCATTCAGCAAGATGATGGAGTGTGAGGAGCA 242
QY 815 TGAAGAGAGCTATCTCCAGCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 874
DB 243 TGAAGAGAGCTATCTCCAGCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302
QY 875 ATGCTGTAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934
DB 303 ATGCTGTAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
QY 935 TTGATGTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
DB 363 TCATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
QY 995 CACTGAGAGCAGCCATTTGCTCCGGGTAAAGGTGTAACAGATTCAGCTGACACC 1054
DB 423 CACTGAGAGCAGCCATTTGCTCCGGGTAAAGGTGTAACAGATTCAGCTGACACC 482
QY 1055 ATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1114
DB 483 ATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542
QY 1115 GGAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1174
DB 543 GGAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
QY 1175 TCGCAGGCTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
DB 603 TAGCTGCTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
QY 1235 GTGACAGAGCTATGTTGAAGCTACCAACAGATCATCAAACTGCTGCTTCCCAAGT 1294
DB 663 GTGACAGAGCTATGTTGAAGCTACCAACAGATCATCAAACTGCTGCTTCCCAAGT 722
QY 1295 CAGAAGTGAAGATATC 1311
DB 723 CAGAAGTGAAGATATC 739

RESULT 14
CB202317 860 bp mRNA linear EST 05-FEB-2003
LOCUS
DEFINITION
CB202317
IMAGE:30141583 5', mRNA sequence.
CB202317
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 860)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. David Rowe

CDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: NDAM049 row: h column: 08
 High quality sequence stop: 637.
 Location/Qualifiers
 1. 860
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 /db_xref="taxon:10090"
 /clone="IMAGE:30141583"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH-MGC_135"
 /note="Vector: pCMVSPORT6.1; Site:1: EcoRV; Site:2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments). Cloned directionally, priming method: Oligo-dT. cDNA normalization: >1x bp, Average insert size 1.6 kb bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'-GACTAGTTTCGATCGGAGCGGCCCTG-3' Tissue contributed by David Rowe. Library constructed by Resgen, Invitrogen Corp."

FEATURES

source

BASE COUNT 225 a 184 c 237 g 214 t
 ORIGIN

Query Match 33.7% Score 574.6; DB 14; Length 860;
 Best Local Similarity 81.4% Pred. No. 4.3e-157;
 Matches 678; Conservative 0; Mismatches 154; Indels 1; Gaps 1;

140 TCCTGTGACCCCTGCTGATAGTGGGATATGATTTGCTTCCAGCCAGAGATTAT 199
 1 TCCTGTGATCTGCTGATATCTGGGTATGAGCTATCTTCCAGCCAGAGATTAT 60
 200 GGTCAAGCTTTAAAAAAGAAATGTTTAAGCTCACAGAGAAATGCCATTATGGCTGA 259
 61 GGTCTGGCTTTAAAAAATTTAAGCTTATCAAGAAATGCCATTATGGAGCTA 120
 260 AGATTCAAGCAAGTTGAACCAAGCAAGATATTTACCAAGCAATGCTATCTCTGA 319
 121 AGATTCAAGCAAGTTGAACCAAGCAAGATATTTACCAAGCAATGCTATCTCTGA 180
 320 AAGTGCACAAAGATATGTAAGAACTTACCTCCAGAGCTGAGCTCATGCTGCTTT 379
 181 AGGTGCACAAAGATATGTAAGAACTTACCTCCAGAGCTGAGCTCATGCTGCTTT 240
 380 TGGAGAACTTAAGAGATACGCTTATGAGAGCTTTGCGCAAGAGGAGAGCTCTG 439
 241 TGGAGAACTTAAGAGATACGCTTATGAGAGCTTTGCGCAAGAGGAGAGCTCTG 300
 440 GAACAGTGTACAGTGGAGAGAGAGCTCACTAGCTCCTTGTGAAGCTTATGAGAGAT 499
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 QY 800 TGGATGAGAGCAAGTGAAGAGACTATCCAGAACTGCGATCTGCTGCTGCTA 859
 Db 661 TGGATGTCAGGCAAGTGAAGAGAGCCATCTCCAGAACTGATGCTGCTGCTGCTA 720
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 Db 721 CCCACAGTTTCTCCATGCTGTAATGATCTGCTGCTCCCGAAGTGGCCAAAGTGGCTGTC 780
 QY 919 AATTCAGAAATACCCCTTCATGTCGACGCTTCTGAGAGCTTCCATCTGAT 971
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RESULT 15

AI701419/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI701419 670 bp mRNA linear EST 18-DEC-1999
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 AI701419
 AI701419.1 GI:4989319
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 670)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/bdrp/image/image.html
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 Location/Qualifiers
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FEATURES

source

/clone_lib="NCI-CGAP-Lu24"
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1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT 183 a 173 c 116 g 198 t
ORIGIN

Query Match 32.7%; Score 558; DB 9; Length 670;
Best Local Similarity 99.8%; Pred. No. 2.8e-152;
Matches 569; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 669 TAGAGATTTTGGAGTATATCT-CACAAAAGCCAGAAATATATGTAATGACATTCACCA 611
   |||||||
QY 107 AGTATGAGCCCTGGCAGCTAATTCAGAGAGTGTCTGTGACCCCTGCTGATAGTCTGGG 166
   |||||||
Db 610 AGTATGAGCCCTGGCAGCTAATTCAGAGAGTGTCTGTGACCCCTGCTGATAGTCTGGG 551
   |||||||
QY 167 GATATGAGTTTGTCTCCAGCCAGAGCTTATGTCAGAGTTTAAAGAAATGTTTA 226
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Db 550 GATATGAGTTTGTCTCCAGCCAGAGCTTATGTCAGAGTTTAAAGAAATGTTTA 491
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QY 227 AGCTCACGAGGAAGATGCCATTATTTGTCGTAAAGTCAAGACAAGTTGAACAAGACCA 286
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Db 490 AGCTCACGAGGAAGATGCCATTATTTGTCGTAAAGTCAAGACAAGTTGAACAAGACCA 431
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Search completed: October 6, 2003, 13:31:11
Job time : 3757 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2003, 08:56:50 ; Search time 6316 Seconds

(Without alignments)
11056.481 Million cell updates/sec

Title: US-10-053-510-7

Perfect score: 1707

Sequence: 1 atgcctagacagacctctc.....gttcctcaaacacactga 1707

Scoring table: IDENTITY_NDC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Genemdb1.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_hcg_hum.*

31: em_hcg_inv.*

32: em_hcg_other.*

33: em_hcg_mus.*

34: em_hcg_pin.*

35: em_hcg_rod.*

36: em_hcg_mam.*

37: em_hcg_vrt.*

38: em_sy.*

39: em_higo_hum.*

40: em_higo_mus.*

41: em_higo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	1707	6 AR220089	AR220089 Sequence
2	1707	100.0	1707	6 AR267065	AR267065 Sequence
3	1707	100.0	1707	6 BD081354	BD081354 Sequence
4	1702.2	99.7	1707	9 AF144638	AF144638 Homo sapi
5	1699	99.5	2130	6 AR282336	AR282336 Sequence
6	1699	99.5	2130	6 AX019488	AX019488 Sequence
7	1699	99.5	2130	6 BD107922	BD107922 Novel com
8	1699	99.5	4701	9 BC052991	BC052991 Homo sapi
9	1699	99.5	5741	9 AB033078	AB033078 Homo sapi
10	1694.2	99.3	2131	9 HSA011304	AJ011304 Homo sapi
11	1297.4	76.0	2033	10 RN0512838	AJ512838 Rattus no
12	1283	75.2	4108	10 BC026135	BC026135 Mus muscu
13	1278.2	74.9	1707	6 AR220088	AR220088 Sequence
14	1278.2	74.9	1707	6 AR267064	AR267064 Sequence
15	1278.2	74.9	1707	6 BD081353	BD081353 Sphingosl
16	1278.2	74.9	1911	10 AF036894	AF036894 Mus muscu
17	1217	71.3	1467	6 AR220092	AR220092 Sequence
18	1217	71.3	1467	6 AR267066	AR267066 Sequence
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23	398.4	23.3	1966	3 DME297394	AJ297394 Caenorhab
24	295.8	17.3	1659	3 AF144639	AF144639 Sequence
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29	256.2	15.0	1770	6 AR267067	AR267067 Sequence
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36	241	14.1	175731	9 AC073176	AC073176 Homo sapi
37	241	14.1	186668	2 AC033639	AC023639 Homo sapi
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39	229.4	13.4	1587	3 AY283052	AY283052 Dictyoste
40	225.6	13.2	1629	6 AR220090	AR220090 Sequence
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ALIGNMENTS

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LOCUS AR220089

SEQUENCE 3 from patent US 6423527.

ACCESSION AR220089

VERSION AR220089.1 GI:23324515

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1707)

AUTHORS Saba,J.D. and Zhou,J.

TITLE Sphingosine-1-phosphate lyase polypeptides, polynucleotides and

modulating agents and methods of use therefor

PATENT: US 6423527-A 3 23-JUL-2002;

JOURNAL

Pred. No. is the number of results predicted by chance to have a

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OY	121	CAGCTAATTCGATGAGAGTGTCTGTGAGACCTGCTGATAGTCTGGGATATGAGTTTCTC	180		
Db	121	CAGCTAATTCGATGAGAGTGTCTGTGAGACCTGCTGATAGTCTGGGATATGAGTTTCTC	180		
OY	181	TTCCAGCCAGAGATTTATGTCAGAGTTTAAAAAGAAATGTTTTAAGCTCACAGGAG	240		
Db	181	TTCCAGCCAGAGATTTATGTCAGAGTTTAAAAAGAAATGTTTTAAGCTCACAGGAG	240		
OY	241	ATGCCCATTTATTTGGTGTAGATTCAAGACAAAGTTGAACAAGACCAAGATGATATTAGC	300		
Db	241	ATGCCCATTTATTTGGTGTAGATTCAAGACAAAGTTGAACAAGACCAAGATGATATTAGC	300		
OY	301	AAGAAATGTCTATTCCTCTGAAAGTGTGACAAAGATATGTGAAGCTTTACCTCCAGGGT	360		
Db	301	AAGAAATGTCTATTCCTCTGAAAGTGTGACAAAGATATGTGAAGCTTTACCTCCAGGGT	360		
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Db	361	CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGCTCATGAGACGCTTCTGG	420		
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OY	481	GTGAAGCTTATGAGATTTTGATGTGAGATTAACCCCTGCATCCAGATATCTTCCAGGA	540		
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Db	901	GTGGCAAGCTGGCTGTGTCAAAATACAAATACCCCTTCATGTGAGAGCTTTGCTGGAGGC	960		

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Db	961	TTCTCATGCTCTTTATGAGAAAGCAGATACCCACTGAGACACCATTGATTTCCGG	1020
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Db	1021	GTGAAAGGTGTAAACAGCATTTTCAGCTGACACCCTAAGTATGCTATGCCCCAAAGGC	1080
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Db	1501	CTAAGAGCAATTCGAGAACTGTACACTCAATCATGAAGATCTTAAAGCAAGACACA	1560
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Db	1561	GGAATGGTGGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1620
OY	1621	TTGCTCTAGTCTTCTTGGAGACGTTGTACAGCAGCAGCAGCAGCAGCAGCAGCAG	1680
Db	1621	TTGCTCTAGTCTTCTTGGAGACGTTGTACAGCAGCAGCAGCAGCAGCAGCAGCAG	1680
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Db	1681	ATGAATGTTCTCCAAAACCCCACTGA	1707
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ACCESSION	AR267065		
VERSION	AR267065.1	GI:29696647	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1707)		
AUTHORS	Saba,J.D. and Zhou,J.		
TITLE	Sphingosine-1-phosphate lyase polypeptides, polynucleotides and modulating agents and methods of use therefor		
JOURNAL	Patent: US 6495359-A 3 17-DEC-2002;		
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ORIGIN

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Db	241	ATGCCCATTTATGTGCTGTAAGATTCAAGACAAAGTGAACCAAGACCAAGATGATTTAGC	300
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Db	361	CTGAGCATCATCTGCTGTTTTGGAGAAACTTAAGGAGTACAGCTCATGAGAGCCCTTCGG	420
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QY	1261	AAACAGATCATCAAAACGTCGCTGCTTCCTCAAGTCAGACACTGGAAATATCAAAAGCATC	1320		
Db	1261	AAACAGATCATCAAAACGTCGCTGCTTCCTCAAGTCAGACACTGGAAATATCAAAAGCATC	1320		
QY	1321	TTTGTGTTTTGGGAATCCCAATTTCTCACTCATTTGCTGTGGATCCGCTGATTTTGGACATC	1380		
Db	1321	TTTGTGTTTTGGGAATCCCAATTTCTCACTCATTTGCTGTGGATCCGCTGATTTTGGACATC	1380		
QY	1381	TACCGACTATCAAAACCTGATGACTGCTTAAGGGGTGGAACCTTGAACCACTTGCACTTCCCA	1440		
Db	1381	TACCGACTATCAAAACCTGATGACTGCTTAAGGGGTGGAACCTTGAACCACTTGCACTTCCCA	1440		
QY	1441	CCCAAGTATTCATTTCTCGATCATACTTACTACGCGCCGGAAGACAGTAGTATACATATTC	1500		
Db	1441	CCCAAGTATTCATTTCTCGATCATACTTACTACGCGCCGGAAGACAGTAGTATACATATTC	1500		
QY	1501	CTAAAGACATTTGAGAACTGTGCATCTCAATCATGAAGAATCTCTAAAGCGAAGACACACA	1560		
Db	1501	CTAAAGACATTTGAGAACTGTGCATCTCAATCATGAAGAATCTCTAAAGCGAAGACACACA	1560		
QY	1561	GGATGGGTGCATCTATGCCATGCGGCGCCACAGCACTTTGACAGGAATATGGTTGCAGAA	1620		
Db	1561	GGATGGGTGCATCTATGCCATGCGGCGCCACAGCACTTTGACAGGAATATGGTTGCAGAA	1620		
QY	1621	TTGTGCTCAGTCTCTTTGGACAGCTTGCTTACAGCACGCACTGTCAACCACAGGCAAGCAG	1680		
Db	1621	TTGTGCTCAGTCTCTTTGGACAGCTTGCTTACAGCACGCACTGTCAACCACAGGCAAGCAG	1680		
QY	1681	ATGAATGGTTCTCCAAAACCCCACTGA	1707		
Db	1681	ATGAATGGTTCTCCAAAACCCCACTGA	1707		
RESULT 3	BD081354	1707 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD081354				
DEFINITION	Sphingosine-1-phosphate lyase polypeptides, polynucleotides and modulating agents and methods of use therefor.				
ACCESSION	BD081354				
VERSION	BD081354.1	GI:22626957			
KEYWORDS	JP 2001518303-A/2.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1707)				
AUTHORS	Saba,J.D. and Zhou,J.				
TITLE	Sphingosine-1-phosphate lyase polypeptides, polynucleotides and modulating agents and methods of use therefor				
JOURNAL	Patent: JP 2001518303-A 2 16-OCT-2001;				
	CHILDREN'S HOSPITAL MEDICAL CENTER OF NORTHERN CALIFORNIA				
COMMENT	OS Unidentified				
	PN	JP 2001518303-A/2			
	PD	16-OCT-2001			
	PF	29-SEP-1998	JP 2000513957		
	PI	29-SEP-1997	US 08/933309		
		JULIE D SABA,JIANHUI ZHOU			

PC C12N15/09, A01K67/027, A61K31/711, A61K38/51, A61K39/395, A61K39/395, A61K45/00, PC A61K48/00, A61P35/00, A61P43/00, C07K16/40, C12N1/21, C12N5/10, PC C12N9/88, PC C12Q1/68, G01N33/15, G01N33/50, C12N15/00, A61K37/56, C12N5/00 CC Strandedness: Single: CC Topology: Linear: CC Sphingosine-1-phosphate lyase polypeptides, polynucleotides CC agents and modulating CC agents and methods of use therefor FH Key Location/Qualifiers 1. 1704. FT CDS 1. 1707. Location/Qualifiers 1. 1707. /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"

BASE COUNT 467 a 388 c 424 g 428 t

ORIGIN

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DB 301 AAGAACATGCTATTTCTGAAAGTGACAAAGATATGTAAGCTTTTACCTCCAGGGT 360
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DB 721 GCCCATGTGCAATTTAACAAAGCAGCAGTACTTTGGGATGAAGATTTGTGGGGTCCCA 780
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DB 1681 ATGAATGTTTCTCAAAAACCCCACTGA 1707

RESULT 4
AF144638 1707 bp mRNA linear PRI 21-JUL-1999
LOCUS Homo sapiens sphingosine-1-phosphate lyase (SPL) mRNA, complete
DEFINITION cds.

ACCESSION AF144638
VERSION AF144638.1 GI:5532486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 1707)
Zhou J. and Saba J.
TITLE Cloning and characterization of human sphingosine-1-phosphate lyase
gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1707)
AUTHORS Zhou J. and Saba J.
TITLE Direct Submission
JOURNAL Submitted (20-APR-1999) Research, Children's Hospital Oakland
Research Institute Oakland Research Institute Oakland, 747 Fifty
Second Street, Oakland, CA 94609-1809, USA
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BASE COUNT 468 a 386 c 425 g 428 t
ORIGIN
Query Match 99.7%; Score 1702.2; DB 9; Length 1707;
Best Local Similarity 99.8%; Freq. No. 0;
Matches 1704; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGCCTAGCAGACCTCTGATGTGAAGCCTTGAGCCCTACTTAGAGATTGTGAA 60
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QY 61 GTATCTCCACAAAAGCCAGAATTTGTAATGACATTCACCAAGTATGAGCCCTGG 120
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QY 121 CAGCTAATTCATGAGTGTGCTGTGACCTGCTGATAGTCTGGGATATGAGTTTTC 180
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Db 1021 GTGAAGGCTTATACAGATTTACAGCTGACACCCATTAAGTATGCTATGCCCAAAAGC 1080
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RESULT 5
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LOCUS AR282336
DEFINITION Sequence 1 from patent US 6521437.
ACCESSION AR282336
VERSION AR282336.1 GI:29718395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2130)
AUTHORS Duckworth,D.M., Godden,R.J. and Testa,T.T.
TITLE Human sphingosine lyase polypeptides
JOURNAL Patent: US 6521437-A 1 18-FEB-2003;
FEATURES
source 1. 2130
BASE COUNT 563 a 479 c 561 g 527 t
ORIGIN

Query Match 99.5%; Score 1699; DB 6; Length 2130;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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LOCUS	AX019488		linear
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ACCESSION	AX019488		
VERSION	AX019488.1	GI:10043420	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Duckworth, D.M., Godden, R.V. and Testa, T.T.		
JOURNAL	Novel sphingosine-1 phosphate lyase		
FEATURES	Patent: WO 938983-A 1 05-AUG-1999;		
SMITHKLINE BEECHAM PLC (GB)			
Location/Qualifiers			
source	1. 2130		
BASE COUNT	563 a	479 c	561 g 527 t
ORIGIN			
Query Match	99.5%;	Score 1699;	DB 6; Length 2130;
Best Local Similarity	99.7%;	Pred. No. 0;	
Matches 1702; Conservative	0;	Mismatches 5;	Indels 0; Gaps 0;
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DB	178	ATGCCCTACACAGACCTCTCTATGTGTGAAGGCGTTTGAGCCCTACTTAGATTTGGAA	237
QY	61	GTATACTCCACAAAAGCCAGAAATTTATGTAAATGACATTGACACCAAGTATGAGCCCTG	120
DB	238	GTATACTCCACAAAAGCCAGAAATTTATGTAAATGACATTGACACCAAGTATGAGCCCTG	297
QY	121	CAGCTAAATTTGATGAGAGTGTGTGTGAGACCCCTGCTGATAGTCTGGGATATGATTTGTC	180
DB	298	CAGCTAAATTTGATGAGAGTGTGTGTGAGACCCCTGCTGATAGTCTGGGATATGATTTGTC	357
QY	181	TTTCAGCCAGAGAGTTTATGTGTCAAGGTTTAAAAAGAAATTTTAAAGCTACACAGAA	240
DB	358	TTTCAGCCAGAGAGTTTATGTGTCAAGGTTTAAAAAGAAATTTTAAAGCTACACAGAA	417
QY	241	ATGCCCATTTATTTGTCGTAAGATTCACACAGTTTGAACAAGACCAAGATGATTTAGC	300
DB	418	ATGCCCATTTATTTGTCGTAAGATTCACACAGTTTGAACAAGACCAAGATGATTTAGC	477
QY	301	AAGAACATGTCATTCCTGAAAGTGACAAAGATGTGAAGGCTTTTACCTCCAGGCT	360
DB	478	AAGAACATGTCATTCCTGAAAGTGACAAAGATGTGAAGGCTTTTACCTCCAGGCT	537

QY	361	CTGAGCTCATCTGCTGTTTGGAGAACTTAAGGAGTACAGCTCATGAGCGCTTCTGG	420
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QY	421	CAAGAGGGAGACGCTCTGGAAAGTGTACAGTGGGGAGGAAAGCTCAGAGCTCTT	480
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QY	481	GTGAAGGCTTATGAGATTTTGCATGTGAGTAAACCCCTGCATATCCATATCTTCCAGGA	540
Db	658	GTGAAGGCTTATGAGATTTTGCATGTGAGTAAACCCCTGCATATCCAGATATCTTCCAGGA	717
QY	541	CTAGCAGATATAGAGCGAGAAATTGTGAGATAGCTTTGCCCTGTTCAATGGGGAGCA	600
Db	718	CTAGCAGATATAGAGCGAGAAATTGTGAGATAGCTTTGCCCTGTTCAATGGGGAGCA	777
QY	601	GATTCGTGTGATGTGTGACTTTCGGGGGAAACAGAAACATATCATAGGCTCGCAAAACA	660
Db	778	GATTCGTGTGATGTGTGACTTTCGGGGGAAACAGAAACATATCATAGGCTCGCAAAACA	837
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Db	898	GCCCATGCTGATTTTACAAAGACAGCCAGTTACTTTGGGATGAAGATTGTGGGGTCCCA	957
QY	781	TTGACGAGATATGATGGAGGTGGATGTGAGGGCAATGAAAGAGCTATCTCCAGGAAACT	840
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DEFINITION Homo sapiens sphingosine-1-phosphate lyase 1, mRNA (cDNA clone
ACCESSION BC052991
VERSION BC052991.1 GI:31418632
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932

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REFERENCE 2 (bases 1 to 4701)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcdg@axil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 110 Row: K Column: 18
This clone was selected for full length sequencing because it
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ORIGIN
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Best Local Similarity 99.7% Pred. No. 0;
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RESULT 9
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VERSION   AB033078.1 GI:6330873
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SOURCE    Homo sapiens
ORGANISM  Homo sapiens (human)
REFERENCE 1 (sites)
AUTHORS   Nagase,T., Ishikawa,K., Kikuno,R., Hirosewa,M., Nomura,N. and Ohara,O.
TITLE     Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
JOURNAL   DNA Res. 6 (5), 337-345 (1999)
MEDLINE   20039619
PUBMED    10574462
REFERENCE 2 (bases 1 to 5741)
AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
TITLE     Direct Submission
JOURNAL   Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
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VYSEEEKTELLIVKAYGDPFAMSNPLHPIDFPGGLKIAEIVRIACSLFENGQPDSCGV
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MEUYRARMARAIISRNTPLMLVCSITPQFPFHGVIDYPRVEAKLVAKIKIPLHNDACIGFLI
IVIEKAKGYPLEHPDFRKYGVTSISADTHVGYGAAPGSSVLVLSIDKRYNRYQFVDFV
DMQGIYASIPFIAGSRPGGISAACMAHLMHGEGSAYEATCOIITARFLKSELENIKK
GIYFVENGPOLISVLIALGSRDPDIYRLSNIMTKGNMLNLOLPPSIHFCITLLHAKRRRA
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BASE COUNT 1369 a 1323 c 1386 g 1663 t

ORIGIN

Query Match	99.5%	Score 1699;	DB 9;	length 5741;
Best Local Similarity	99.7%;	Pred. NO. 0;		
Matches 1702;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0;

OY	1	ATGCCCTACACAGACCTCTGTGATGTTTGAAAGGCTTTGAGCCCTACTTAAAGATTTTGGAA	60
Db	201	ATGCCCTACACAGACCTCTGTGATGTTTGAAAGGCTTTGAGCCCTACTTAAAGATTTTGGAA	260
OY	61	GTATCTCTCCAAAAGCCAGAATTAATGTAATGGACATTTGCACCAAGTATGAGCCCTGG	120
Db	261	GTATCTCTCCAAAAGCCAGAATTAATGTAATGGACATTTGCACCAAGTATGAGCCCTGG	320
OY	121	CAGCTAAATTCATGAGAGTGTCTGTGGAGACCTCGCTGATATGTCTGGGGATATGAGTTTGTCT	180
Db	321	CAGCTAAATTCATGAGAGTGTCTGTGGAGACCTCGCTGATATGTCTGGGGATATGAGTTTGTCT	380
OY	181	TTCCAGCCAGAGAGTTTATGTGTCAAGGTTTAAAAAGAAATGTTTAAAGCTCACACAGAGAG	240
Db	381	TTCCAGCCAGAGAGTTTATGTGTCAAGGTTTAAAAAGAAATGTTTAAAGCTCACACAGAGAG	440
OY	241	ATGCCCATTAATTTGGTCGTATAGATTCGAAGCAAGCAAGTTCGAACAACCAACGAAGTATATTAGC	300
Db	441	ATGCCCATTAATTTGGTCGTATAGATTCGAAGCAAGTTCGAACAACCAACGAAGTATATTAGC	500
OY	301	AAGAACATGTCTCATTTCTGTAAGATGGACAAGAGATATGTCAAAAGCTTTACCCTCCACAGGT	360
Db	501	AAGAACATGTCTCATTTCTGTAAGATGGACAAGAGATATGTCAAAAGCTTTACCCTCCACAGGT	560
OY	361	CTGAGCTCATCTGCTGTTTGTGGAGAACTTAAAGAGTACAGCTCTATGGACGCTTCTGG	420
Db	561	CTGAGCTCATCTGCTGTTTGTGGAGAACTTAAAGAGTACAGCTCTATGGACGCTTCTGG	620
OY	421	CAAGGGGAGAGAGCCCTCGGAACAGTGTACAGTGGGGAGAGAGAGCTCACTGAGCTCTG	480
Db	621	CAAGGGGAGAGAGCCCTCGGAACAGTGTACAGTGGGGAGAGAGAGCTCACTGAGCTCTG	680
OY	481	GTGAAGGCTTATGAGAGATTTTGCATGAGAGTAAACCCCTGCATCCACATATCTTCCAGGA	540
Db	681	GTGAAGGCTTATGAGAGATTTTGCATGAGAGTAAACCCCTGCATCCACATATCTTCCAGGA	740
OY	541	CTAGCAAGATAGAGGCAAAATTGGAGAGATAGCTGTCTCCCTGTTCATAGGGGGAGCA	600
Db	741	CTAGCAAGATAGAGGCAAAATTGGAGAGATAGCTGTCTCCCTGTTCATAGGGGGAGCA	800
OY	601	GATTGCTGTGATGTTGTGACTTCTGGGGGAGACAGAAAGCATACTCATGCGCTGCAAGCA	660
Db	801	GATTGCTGTGATGTTGTGACTTCTGGGGGAGACAGAAAGCATACTCATGCGCTGCAAGCA	860
OY	661	TGTCGGGATCTGGCCTTTGAGAGGGGATCAAAATCTCCAGAAATTTGGCTCCCCAAAGT	720
Db	861	TATCGGGATCTGGCCTTTGAGAGGGGATCAAAATCTCCAGAAATTTGGCTCCCCAAAGT	920

QY	721	CCCATGGTGCATTTAAACAAAGCAGCCAGTACTCTTTGGGATGAGATTTGGCGGCTCCCA	780
Db	921	GCCCCATGGTGCATTTAAACAAAGCAGCCAGTACTCTTTGGGATGAGATTTGGCGGCTCCCA	980
QY	781	TTGACGAAGATGATGAGAGGTGGATGTGAGGGCACTGAGAAGAGCTATCTCCAGGAACT	840
Db	981	TTGAGGAAGATGATGAGAGGTGGATGTGAGGGCACTGAGAAGAGCTATCTCCAGGAACT	1040
QY	841	GCCATGCTCGTCTGTTCTACCCCAACAGTTTCTCATGCTGTAATAGATCTGTCCCTGAA	900
Db	1041	GCCATGCTCGTCTGTTCTACCCCAACAGTTTCTCATGCTGTAATAGATCTGTCCCTGAA	1100
QY	901	GTGGCGCAAGCTGGCGTGCATACAAATAATACCCCTCATGTCGACGCTTGTGCTGGGAGC	960
Db	1101	GTGGCGCAAGCTGGCGTGCATACAAATAATACCCCTCATGTCGACGCTTGTGCTGGGAGC	1160
QY	961	TTCCCTCATCGCTCTTTATGAGAGAAGCAGAGATACCACCTGAGCAGCACCATTGATTTCCGG	1020
Db	1161	TTCCCTCATCGCTCTTTATGAGAGAAGCAGAGATACCACCTGAGCAGCACCATTGATTTCCGG	1220
QY	1021	GTGAAGGTGTACCCAGCATTTCAGCTGACACCCATAAGTATGCGTATGCCCCAAAAGGC	1080
Db	1221	GTGAAGGTGTACCCAGCATTTCAGCTGACACCCATAAGTATGCGTATGCCCCAAAAGGC	1280
QY	1081	TCATCATTTGGTGTTGATAGTACGAAAGAGTACAGAACTATCAGTTCTTCTGCTGATACA	1140
Db	1281	TCATCATTTGGTGTTGATAGTACGAAAGAGTACAGAACTATCAGTTCTTCTGCTGATACA	1340
QY	1141	GATTGGCAGGGTGCATCTATGCTTTCCCAACATCCAGGCTCAGCGGCTCGTGGCATTT	1200
Db	1341	GATTGGCAGGGTGCATCTATGCTTTCCCAACATCCAGGCTCAGCGGCTCGTGGCATTT	1400
QY	1201	AGCGCAGCCTTTGGGCGTCCCTGTATGCACTTTCGGGTGAGAACCGGCTATGTTGAAGCTAAC	1260
Db	1401	AGCGCAGCCTTTGGGCGTCCCTGTATGCACTTTCGGGTGAGAACCGGCTATGTTGAAGCTAAC	1460
QY	1261	AAACAGATCATCAAAACAGTCTCGGCTTCCTCAAGTCAGAACGTAAGTATCAAAAGCATC	1320
Db	1461	AAACAGATCATCAAAACAGTCTCGGCTTCCTCAAGTCAGAACGTAAGTATCAAAAGCATC	1520
QY	1321	TTTGTGTTTTGGGAAATCCCAAAATGTGCACTCATTTGCTCTGGGATCCCGTGATTTTGACATC	1380
Db	1521	TTTGTGTTTTGGGAAATCCCAAAATGTGCACTCATTTGCTCTGGGATCCCGTGATTTTGACATC	1580
QY	1381	TAACGACATCAAAACGTCGATGACGTCGTAAGGGGTGAGAACTGAAACGATTCGAACTCCCA	1440
Db	1581	TAACGACATCAAAACGTCGATGACGTCGTAAGGGGTGAGAACTGAAACGATTCGAACTCCCA	1640
QY	1441	CCCGATATTCATTTCTCGCATCACATTTACTACACGCCCGGAAACAGATAGCTATCAAAATTC	1500
Db	1641	CCCGATATTCATTTCTCGCATCACATTTACTACACGCCCGGAAACAGATAGCTATCAAAATTC	1700
QY	1501	CTAAAGCAGATTCGAGAACTGTGCACTCAATCATATGAAGATCTTAAAGGAGAGACCACA	1560
Db	1701	CTAAAGCAGATTCGAGAACTGTGCACTCAATCATATGAAGATCTTAAAGGAGAGACCACA	1760
QY	1561	GGAATGGGTGCATCTATGCGCATGAGCCAGACCACTGTGACAGGAATATGTTGCGAATA	1620
Db	1761	GGAATGGGTGCATCTATGCGCATGAGCCAGACCACTGTGACAGGAATATGTTGCGAATA	1820
QY	1621	TTGTGCTCAGTCTCTTGGAGACGTTGTACAGCAGCACTGTCAACCGAGGCGAGCAG	1680
Db	1821	TTGTGCTCAGTCTCTTGGAGACGTTGTACAGCAGCACTGTCAACCGAGGCGAGCAG	1880
QY	1681	ATGAATGGTGTCTCCAAAACCCCACTGA	1707
Db	1881	ATGAATGGTGTCTCCAAAACCCCACTGA	1907

RESULT 10	
HSA011304	
LOCUS	
DEFINITION	HSA011304 2131 bp mRNA linear PRI 14-SEP-2000
	Homo sapiens mRNA for sphingosine-1-phosphate lyase.

RESULT 11	
RN0512838	
LOCUS	RN0512838
DEFINITION	2033 bp mRNA linear ROD 25-OCT-2002
ACCESSION	RN0512838
VERSION	AJ512838.1 GI:24412854
KEYWORDS	sphingosine-1-phosphate lyase; spl gene.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 Van Veldhoven, P.P.
TITLE	Comparison of sphingosine-1-phosphate lyases
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2033).
AUTHORS	Van Veldhoven, P.P.
TITLE	Direct Submission
JOURNAL	Submitted (24-OCT-2002) Van Veldhoven P.P., Farmakologle, K.U.Leuven, Herestraat, B-3000 Leuven, BELGIUM
FEATURES	Location/Qualifiers
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gene	
CDS	

BASE COUNT	544	a	472	c	528	g	489	t
ORIGIN								
Query Match	76.0%: Score 1297.4; DB 10; Length 2033;							
Best Local Similarity	85.0%: Pred. No. 0;							
Matches 1451: Conservative	0; Mismatches 256; Indels 0; Gaps 0;							
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DB	130	ATGCCGAGTACCGACACTTCTCAAGTTGAAGCACTTCAGCCTTATT	TGGAGATTTTGGAA	189				
QY	61	GTATATCTCCACAAAAGCCAGAAATTATGTAATGAGCACTTGCACCAAGTATAGCCCTGG	120					
DB	190	GCAATATTCACAAAAGCCAAAGAAATTAGCTGATGAGTACCTGCACCAATATAGCAACCTCGG	249					
QY	121	CAGCTAATTTGATGAGAGTGTGCTGGACCCCTGCTGATAGCTGGGGATATGATTTGTC	180					
DB	250	CAGCTCATGTGGGGAGTGTCTCTGTACTCTGCTGATGCTGGATATATAGCACTTATC	309					
QY	181	TTCCAGCCAGAGATTTATGGTCAAGGTTTAAAAAGAAATTTTTAAAGCTCCACAGAG	240					
DB	310	TTCCAGCCAGAGATTTATGGTCTCGGTTTAAAAATTAATTTATTTAGCCTTATAAGAG	369					
QY	241	ATGCCCATTTATGTGCTGATAGATTCAAGACAAAGTTGAACAAGCAACCAAGATGATTAAGC	300					
DB	370	ATGCACTTTATTTAGACCAATAGATACAAACAGCAGCTTACCAAGCCAAAGAAAGATCTGTGC	429					
QY	301	AAGAAACATGTCATCTCGAAAGTGGACAAAGATGTAAGAAAGCTTTAACCTCCAGGCT	360					
DB	430	AAGAAACATGCTTCCTCGAAAGTTGGACAAAGATTTATGTGAACACCTGCTGTACAGGCT	489					
QY	361	CTGAGACATATGCTGTGTTTGAAGAAACTTTAAGAGATACAGCTTATGAGACCTTCTG	420					
DB	490	CTGAGACAGCTGAGGTTCTGAGAGACACTCAAGAGATACAGCTTCATGATGTCTTCTGG	549					
QY	421	CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAAAGCTTACATGAGCTCCTT	480					
DB	550	CAAGAGGGAGAGCCTCAGAGAGCTGTGTACAGTGGGGAGCGGAAGCTCACGAGCTGCTG	609					
QY	481	GTGAAGCTTATGAGATTTTGCATGGAATTAACCCCTGCAATCCAGATATCTTCCACAGA	540					
DB	610	GTGAGAGCTTATGAGAAATTCACGTGGAGCAATCCACTGCACCCAGATATCTTCCCGGA	669					
QY	541	CTAGCAAGATAGAGGAGCAAAATTTGTGAGATAGCTTTTCCCTGTTCAATGGGGAGCA	600					
DB	670	CTAGGGAAGTTAGAGGAGCAAAATGTGAGAGATGACTTGTCTCTTCAATGGGGAGCA	729					
QY	601	GATTCTGTGTGATGTGTGACTTCTGTGGGGAGACAGAAAGCATATCATGAGCCTGCAGAA	660					
DB	730	GACTCTGTGTGATGTGTGACTTCTGTGGGGAGACAGAAAGCATATCATGAGCCTGCAGAA	789					
QY	661	TGTGGGATCTGTGGCTTTGAGAAAGGGATCAAAACTCCAGAAATTTGTGTCTCCCAAGT	720					
DB	790	TATGGGGACTTGTGGCTTTAGAGAAAGGGATCAAAACTCCAGAAATTTGTGTCTCCAGAGT	849					
QY	721	GCCCATGCTGATTTAAACAAGACGCCACTACTTTGGAGTGAAGATGTGCGGGTCCCA	780					
DB	850	GCCCAAGCCGCTATTCAGACAAAGCAAGCTCATTTATTTCCGATATGAAGATTTGTACGGCTTGGC	909					
QY	781	TTGACGAAGATGATGAGAGTGTGATGTGAGGCAATGAAAGAGCTATCTCCAGAGAACT	840					
DB	910	CAGAAAAAGACATGAGAGTGTGATGTGGGGCAATGAAAAAGAGCATCTCCAGGAACCA	969					
QY	841	GCCATGCTGTCTTCTTACCCACAGTTTCTCATGGTGAATAGATCTGTCTCCAGAA	900					

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BASE COUNT 1008 a 947 c 1033 g 1120 t

Query Match 75.2% Score 1283; DB 10; Length 4108;
Best Local Similarity 84.5% Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

QY 1 ATGCGTAGCAGACCTTCTGATGTTGAAGCCCTTTGAGCCCTTCTAGAGATTGGA 60
DB 137 ATGCGCGGAGACCGACCTCTCAAGCTGAGAGACTTCAGCCTTATTTGGAGATTGGA 196
QY 61 GTATCTCCACAAAAGCCAAAGATTATGTAATGACATTGACCAAGATAGACCCCTG 120
DB 197 TCATATTCACAAAAGCCAAAGATTATGTAATGATTTGACCAATATAGACCCCTG 256
QY 121 CAGTATTCAGTAGAGTGTGCTGTGAGCCCTGCTGATGCTGAGGATATGATTTGTC 180
DB 257 CAGCTATTCAGTAGAGTGTGCTGTGAGCTGCTGATGCTGAGGATATGATTTGTC 316
QY 181 TTCCAGCCAGAGAGTTTATGCTCAAGCTTTAAAGAAATGTTTAACTCACAGAGAG 240
DB 317 TTCCAGCCAGAGAGTTTATGCTCGGTTTAAAGAAATATTTAACTTATCAGAGAG 376
QY 241 ATGCCCATTTATGCTCTAAGATTCAAGACAGTTGAACAAGACAGATGATTTAGC 300
DB 377 ATGCCCATTTATGCTCTAAGATTCAAGACAGTTGAACAAGACAGATGATTTAGC 436
QY 301 AAGAACATTCATTCCTGAAGAGTGAAGAGATATGTAAGCTTATACCTCCAGAGT 360
DB 437 AAGAACATTCATTCCTGAAGAGTGAAGAGATATGTAAGCTTATACCTCCAGAGT 496
QY 361 CTGAGCTCATCTGCTGTTTGAAGAACTTAAAGAGTACAGCTTATAGAGCCCTTGG 420
DB 497 ATGGGACAGCTGAGTGTCTGAGAGACTCAAGAGATACAGCTTATAGAGTCTGCTG 556
QY 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGTCACTGAGCTCTT 480
DB 557 CAAGAGGGAGAGCCTCTGGAACAGTGTGTACATGGGAGACCAAGAGTCACTGAGCTCTG 616
QY 481 GTGAAGCTTATGAGATTTTGTGATGAGTAAACCCCTGATCCAGATTTCTCCAGGA 540
DB 617 GTGAGGCTTATGAGATTTTGTGATGAGTAAACCCCTGATCCAGATTTCTCCAGGA 676
QY 541 CTACGCAAGATAGAGCAGAAATTTGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
DB 677 TTGGGAGATTTAGAGAGAGAAATGTTAGATGATCTTCCCTTCAATGGGGAGCA 736
QY 601 GATTCGTGTGAGTGTGACTTCTGGGGAGACAGAAACATCTCATGAGCCCTGCAAGCA 660
DB 737 GATTCGTGTGAGTGTGACTTCTGGGGAGACAGAAACATCTCATGAGCCCTGCAAGCA 796
QY 661 TTGCGGATCTGCGCTTTGGAAGAGGATCAAAATCTCAGAAATTTGGCTCCCAAGT 720
DB 797 TACCGGAGCTTGGCTTTGAGAGAGGATCAAAATCTCAGAAATTTGGCTCCCAAGT 856
QY 721 GCCCATGCTGATTTAAACAAGCAGCAGTTACTTTGGAGTGAAGATTTGGCGGAGCA 780
DB 857 GCCCATGCTGATTTAAACAAGCAGCAGTTACTTTGGAGTGAAGATTTGGCGGAGCA 916
QY 781 TTGACGAAGATGATGAGGTGATGTAGAGGCAATGGAAGAGCTATCTCCAGGAACAT 840
DB 917 CTGAAAAAGAAACATGAGGTGATGTAGAGGCAATGGAAGAGCTATCTCCAGGAACAT 976
QY 841 GCCATGCTGCTGCTTTTACCCCACTTTCTCATATGTTGAATGATCTGCTGCTGGA 900
DB 977 GCTATGCTGCTGCTTTTACCCCACTTTCTCATATGTTGAATGATCTGCTGCTGGA 1036

QY 901 GTGGCCAGCTGGCTGTCAATAACAAATACCCCTTCATGTGACGCTGTGTGGAGCC 960
DB 1037 GTGGCCAGATTTGGCTGTGACATATTAATATCCACTCATGATGATGCTGTGTGGAGCC 1096
QY 961 TTCTCTATGCTTTTATGAGAAAGCAGATACCAGTACAGCAGCAGCAGCAGCAGCAG 1020
DB 1097 TTCTCTATGCTTTTATGAGAAAGCAGATACCAGTACAGCAGCAGCAGCAGCAGCAG 1156
QY 1021 GTGAAGGTTAAACACATTTTCAAGACACCATTAAGTATGCTTATGCCCCAAAGGC 1080
DB 1157 GTGAAGGTTAAACACATTTTCAAGACACCATTAAGTATGCTTATGCCCCAAAGGC 1216
QY 1081 TCATCATGCTGTGTGTATGATGACAAAGATACAGAACTATCATCTTCTGCTGATACA 1140
DB 1217 TCATCATGCTGTGTGTATGATGACAAAGATACAGAACTATCATCTTCTGCTGATACA 1276
QY 1141 GATTGCAAGGTGAGCTATGCTTCCCAACCATCTCCAGGCTCAGGCTGTGGCATTT 1200
DB 1277 GACTGGCAAGGTGAGCTATGCTTCCCAACCATCTCCAGGCTCAGGCTGTGGCATTT 1336
QY 1201 AGCGCAGCTGTGGGCTGGCTGTGACACATCTGAGTGAAGAGGCTATGTTGAAGCTACC 1260
DB 1337 ATTCAGCTGTGTGGGCTGGCTGTGACACATCTGAGTGAAGAGGCTATGTTGAAGCTACC 1396
QY 1261 AACAGATCATCAAAACTGCTGCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1320
DB 1397 AACAGATCATCAAAACTGCTGCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1456
QY 1321 TTGCTTTTGGGAATCCCAATTTGCTACTATTCCTGTGGAGTCCGCTGATTTGACATC 1380
DB 1457 TTGCTTTTGGGAATCCCAATTTGCTACTATTCCTGTGGAGTCCGCTGATTTGACATC 1516
QY 1381 TACCGATATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1517 TACCGATATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
QY 1441 CCCAGTATTCATTTCTCATACATCTACACAGCCCGGAAACAGTATGATATCAATTC 1500
DB 1577 AGAAGCATTTCTTCTCATACATCTACACAGCCCGGAAACAGTATGATATCAATTC 1636
QY 1501 CTAAAGCAATTCGAGATCTGCTACATCAATCTATGAAGATCTTAAAGCAAGACACA 1560
DB 1637 CTAAAGCAATTCGAGATCTGCTACATCAATCTATGAAGATCTTAAAGCAAGACACA 1696
QY 1561 GGAATGGGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1697 GGAATGGGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1756
QY 1621 TTGCTCTCAGTCTCTTGAAGAGTGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1680
DB 1757 ATATCTCTCAGTCTCTTGAAGAGTGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1836
QY 1681 ATGAATGTTCTCCAAACCCCACTGA 1707
DB 1817 ATGAACGTTCTCCAAACCCCACTGA 1843

RESULT 13
AR220088
LOCUS 1707 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6423527.
ACCESSION AR220088
VERSION AR220088.1 GI:23324514
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1707)
AUTHORS Saba J.D. and Zhou J.
TITLE Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
modulating agents and methods of use therefor
JOURNAL Patent: US 6423527-A 1 23-JUL-2002;
FEATURES location/Qualifiers


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source      1. .1707
            /organism="unknown"
BASE COUNT  460 a      376 c      440 g      431 t
ORIGIN
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Query Match	74.9%;	Score 1278.2;	DB 6;	Length 1707;
Best Local Similarity	84.3%;	Pred. No. 0;		
Matches 1439; Conservative	0;	Mismatches 268;	Indels 0;	Gaps 0.

QY	1	ATGCGTCAGACAGACGCTTCTGATGTGTTGAAGGCTTTGAGCCCTTACGATTAATTTGGAA	60
Db	1	ATGCGCGGAACCGACCTCTCTCAAGCTGAAGGACCTTCAGGCTTTTGGAGATTTTGGAA	60
QY	61	GTATACTCCAAAAAGCCCAAGATTATGTAAATGACATTGGCACCAAGATATGAGCCCTGG	120
Db	61	TCTTATTCCAAAAAGCCCAAGATTATGTGAATGGATTTTGCACCAATATATGAGCCCTGG	120
QY	121	CAGCTAATTGCAATGGAAGTGTGCTGTGGACCTGCTGATAGTCTGTGGGATATGAGTTTGTG	180
Db	121	CAGCTATTGCGGGAGTGCTGTGTACTGTGCTGTGATGATCTGGGGATATGAGCTTATG	180
QY	181	TTTCGACCCAGAGAGTTTATGTGTCAGAGTTTAAAAAGAAATGTTTAAAGTCACACAGAG	240
Db	181	TTTCACACAGAGAGTTTATGTGCTGTGGTTTAAAAAAAATATTATTTAAGCTTATACAGAG	240
QY	241	ATGCCATTATTGGTGTGAAGATTCAAGACAAAGTTGAACAAGCAAGATGATATTAGC	300
Db	241	ATGCCATTATTGGAGCTAGCATGCACACACAGAGTAGACAAAGCCAAAGAAAGATCTTGTC	300
QY	301	AAGCAATGTCACTTCTTGAAAGTGGACAAAGNRTGTGAAAGCTTTACCTCCAGAGT	360
Db	301	AAGCAATCCATCTCTAAAGGTGACAAAGATTATGGAATACTGCTGCTCAGAGT	360
QY	361	CTGAGCTCATCTGCTGTTTGGAGAAATTAAAGAGTACAGCTATGACAGCCTTTG	420
Db	361	ATGGGACACAGCTGAGGTTCTGTGAGAGACTCAAGAGTAGTACAGTCAATGATGTTCTGTG	420
QY	421	CAAGAGGGAGAGCCTCTGGAACACTGTACAGTGGGGAGAGAAAGTCACTGAGCTCTT	480
Db	421	CAAGAAAGGGAAGGCTCAGAGAGCTGTGTACATATGGGGAACGGAAGCTCACGGAGCTGTG	480
QY	481	GTCAGGCTTATGAGAGATTTCGATGAGGTAACCCCTGCATCCAGATATCTTCCACGA	540
Db	481	GTCAGGCTTATGAGAGATTTCAGCGGAGCAATCCACTGCATCCAGATATCTTCCCTGGA	540
QY	541	CTACGCAATATAGAGGCAAGAAATTTGAGAGTAGCTTTCCTGTTCAATGGGGGACCA	600
Db	541	TTTCGGAAATTTAGAGGCAAGAAATCTGTAGGATGACTTGTCCCTTCAATGGGGGACCA	600
QY	601	GATTCGTGTGATGTGTGACTTCTGGGGGAAACAGAAACATATCATGAGGCTGCAGAACCA	660
Db	601	GATTCGTGTGATGTGTGACTTCTGGGGGAAACGAAACATCTGATGGGCTGCAGAAAGCT	660
QY	661	TGTCCGGATCTGGGCTTTGAGAAAGGGATCAAAAATCTCAGAAATTTGGCTCCCGAAGT	720
Db	661	TACCGGGAATTTGGGCTTTAGAGAAAGGGATCAAAAATCTCAGAAATTTGGCTCCCGAAGT	720
QY	721	GCCCATGCTGCAATTTAAACAAAACACAGCAGTTACTTTGGGATGAAGATTTGGCGGATCCA	780
Db	721	GCCCATGCTGCAATTTGACAAAGCAGCTATTTATTTTGGGATGAAGATTTGTCGAGTTGCA	780
QY	781	TTGACGAGAGATGATGAGAGTGTGATGAGGGCAATGAGAAAGAGTATCTCCAGAAACT	840
Db	781	CTGAAAGAAACATGAGAGTGTGATGCAAGGCATATGAAGAGCCATCTCCAGAAACACA	840
QY	841	GCAATGCTGTCTGTCTTAACCCACAGTTTCTCATGTGTGATGATGATCTGTCCCGAA	900
Db	841	GCAATGCTGTCTGTCTTAACCCACAGTTTCTCATGTGTGATGATGATCTGTCCCGAA	900
QY	901	GTCGGCAACCTGGCTGATAAATATCAAAATATCCCTTCATATGCGAGGTTTCTGTGGAGGC	960
Db	901	GTCGGCAAGTTTAAGTCTGATATTAATATCCCACTTCATATGAGATGCTGTGTGGGGGGC	960

Oy	961	TTCCATCGCTTTATGAGAAAGACAGGATATACCAGTCGGAGCCATTTGATTTCGG	1020
Db	961	TTCCATCGCTTTATGAGAAAGACAGGATATACCAGTCGGAGCCATTTGATTTCGG	1020
Oy	1021	GTGAAGGTTAACGACATTTCAGCTGACACCCATAAGTATGCGTATGCCCAAAAGC	1080
Db	1021	GTGAAGGTTAACGACATTTCAGCTGACACCCATAAGTATGCGTATGCCCAAAAGC	1080
Oy	1021	GTGAAGGTTAACGACATTTCAGCTGACACCCATAAGTATGCGTATGCCCAAAAGC	1080
Db	1021	GTGAAGGTTAACGACATTTCAGCTGACACCCATAAGTATGCGTATGCCCAAAAGC	1080
Oy	1081	TCATCATTTGGTGTATAGTACAGAAAGTACAGAAAGTATTCAGTCTTCGTGATACA	1140
Db	1081	TCATCATTTGGTGTATAGTACAGAAAGTACAGAAAGTATTCAGTCTTCGTGATACA	1140
Oy	1141	GATTGGCAGGSGTCATCTATGCTTTCCCAACCATTCGACAGGCTACGCGCTGTGGCATT	1200
Db	1141	GATTGGCAGGSGTCATCTATGCTTTCCCAACCATTCGACAGGCTACGCGCTGTGGCATT	1200
Oy	1201	AGCGCAGCCTTGTGGGCTGCTTATGACACTTCGGGTGAGAAAGGCTATGTTGAAGTACC	1260
Db	1201	AGCGCAGCCTTGTGGGCTGCTTATGACACTTCGGGTGAGAAAGGCTATGTTGAAGTACC	1260
Oy	1261	AAACAGATATCAACAACCTGCTCGGCTTCCTCAAGTCAGACGTAAGTAATATCAAGGATC	1320
Db	1261	AAACAGATATCAACAACCTGCTCGGCTTCCTCAAGTCAGACGTAAGTAATATCAAGGATC	1320
Oy	1321	TTTGTTTTTGGGAATCCCAATTGCTACATCTATGCTCTGGGATCCGCTGATTTTGACATC	1380
Db	1321	TTTGTTTTTGGGAATCCCAATTGCTACATCTATGCTCTGGGATCCGCTGATTTTGACATC	1380
Oy	1381	TACCGACTATCAAAACCTGATGACGTCGTAAGGGGTGGAACCTGAAACCGATTGCTCCCA	1440
Db	1381	TACCGACTATCAAAACCTGATGACGTCGTAAGGGGTGGAACCTGAAACCGATTGCTCCCA	1440
Oy	1441	CCGAGTATTCATTTCTGCATCACAATTACTACACGCCCGGAAACGAGTAGTATACAAATC	1500
Db	1441	CCGAGTATTCATTTCTGCATCACAATTACTACACGCCCGGAAACGAGTAGTATACAAATC	1500
Oy	1501	CTAAGAGCATTTGAGAAATGTCGATCACTCAATATCTAGAAAGATCCTAAGGAAGACACA	1560
Db	1501	CTAAGAGCATTTGAGAAATGTCGATCACTCAATATCTAGAAAGATCCTAAGGAAGACACA	1560
Oy	1561	GGAATGGGTGCATCTATGCGCATGGCCAGCAACACTGTCAGAGGAATATGTTGACGAA	1620
Db	1561	GGAATGGGTGCATCTATGCGCATGGCCAGCAACACTGTCAGAGGAATATGTTGACGAA	1620
Oy	1621	TTTGTCCTCAGCTCTTCTTGACAGCTTGTACAGCACCGACACTGTACCCAGGACGACAG	1680
Db	1621	TTTGTCCTCAGCTCTTCTTGACAGCTTGTACAGCACCGACACTGTACCCAGGACGACAG	1680
Oy	1681	ATGATGAGTCTCCAAAACCCCACTGA	1707
Db	1681	ATGATGAGTCTCTCCAAAACCCCGCTGA	1707
RESULT 14			
LOCUS	AR267064	1707 bp	DNA
DEFINITION	Sequence 1 from patent US 6495359.	linear	PAT 10-Apr-2003
ACCESSION	AR267064		
VERSION	AR267064.1	GI:29696646	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1707)		
AUTHORS	Saba,J.D. and Zhou,J.		
TITLE	Splipposine-1-phosphate lyase polypeptides, polynucleotides and		
JOURNAL	modulating agents and methods of use therefor		
FEATURES	Patent: US 6495359-A 1 17-DEC-2002;		
FEATURES	Location/Qualifiers		
SOURCE	1..1707		
BASE COUNT	460 a	376 c	440 g
ORIGIN			431 t

Query Match 74.9%; Score 1278.2; DB 6; Length 1707;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

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DB 781 TTGACGAGATGATGAGTGTGAGTGTGAGGAGCAATGAGAGATCTCAGAGAACT 840
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DB 901 GTGCGCAGCTGCTGTCAAAATACCCCTTATGTCAGAGCTTGTCTGGAGGC 960
QY 961 TTGCTCATGCTTATGAGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TTGCTCATGCTTATGAGAGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAG 1020
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QY 1081 TCATCATTTGTTGTTATATGATGACAGAGATACAGAGATCATATGATTTCTGTCATACA 1140
DB 1081 TCATCATTTGTTGTTATATGATGACAGAGATACAGAGATCATATGATTTCTGTCATACA 1140
QY 1141 GATTGAGAGGTGATCTATGCTTCCCAACATGTCAGAGCTGAGGCTGGGGGATTT 1200
DB 1141 GATTGAGAGGTGATCTATGCTTCCCAACATGTCAGAGCTGAGGCTGGGGGATTT 1200
QY 1201 AGCGACAGCTGTTGGGCTGCTTATGATGACATTCGTTGAGAGAGAGCTATTTGAAAGTACC 1260
DB 1201 AGCGACAGCTGTTGGGCTGCTTATGATGACATTCGTTGAGAGAGAGCTATTTGAAAGTACC 1260
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DB 1261 AAACAGATCATCAAAACTGCTCGCTTCTCAAGTACAGACTGCAAAATATCAAAAGCATC 1320
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DB 1321 TTTGTTTGGGAAATCCCAATTTGTCATGATGCTGAGATCCGCTGATTTTGCATC 1380
QY 1381 TACGACTATCAAACTGATGATGCTTAAGGGGTGAACTTGAACAGCTTGCAGTTCCCA 1440
DB 1381 TACGACTATCAAACTGATGATGCTTAAGGGGTGAACTTGAACAGCTTGCAGTTCCCA 1440
QY 1441 CCAGATTTTATTTTGTGATCATATTAATCTACAGCCCGGAAAGAGATGATTAATCAATTC 1500
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DB 1501 CTAAAGGATCTTGGAGATGTCATGATCAATGATGAAGATCTTAAGGAGAGAGACCA 1560
QY 1561 GGAATGGGTGCAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 GGAATGGGTGCAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 TTGCTCTCATGCTTCTTGGAGAGCTTGTACAGCAGCAGCATCTGACCCAGGAGCAG 1680
DB 1621 TTGCTCTCATGCTTCTTGGAGAGCTTGTACAGCAGCAGCATCTGACCCAGGAGCAG 1680
QY 1681 ATGAGTGTCTTCCAAAACCCCACTGA 1707
DB 1681 ATGAGTGTCTTCCAAAACCCCACTGA 1707

RESULT 15
BD081353 1707 bp DNA linear PAT 27-AUG-2002
LOCUS Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
DEFINITION modulating agents and methods of use therefor.
ACCESSION BD081353
VERSION BD081353.1 GI:22626956
KEYWORDS JP 2001518303-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1707)
AUTHORS Saba,J.D. and Zhou,J.
TITLE Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
modulating agents and methods of use therefor
JOURNAL Patent: JP 2001518303-A 1 16-OCT-2001;
CHILDREN'S HOSPITAL MEDICAL CENTER OF NORTHERN CALIFORNIA
OS Unidentified
PN JP 2001518303-A/1
PD 16-OCT-2001
PF 29-SEP-1998 JP 2000513957
PR 29-SEP-1997 US 08/939309
PC JUIE D SABA, JIANHUI ZHOU
C12M15/09,A01K67/027,A61K31/711,A61K38/51,A61K39/395,A61K39/
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2003, 10:29:21 : Search time 478 Seconds
(without alignments)
9640.043 Million cell updates/sec

Title: US-10-053-510-7
Perfect score: 1707
Sequence: 1 atgcctagacagacctctt.....gttcctcaaacaccactga 1707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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25: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1707	100.0	1707	20	AAK25567	Human sphingosine-
2	1702.2	99.7	1707	24	ABLS59529	Human sphingosine-
3	1699	99.5	2130	20	AAZ06342	Sphingosine-1-phos
4	1699	99.5	2446	22	AAK51594	Human polynucleoti
5	1697.4	99.4	2093	22	AAK52578	Human polynucleoti
6	1278.2	74.9	1707	20	AAK25366	Mouse sphingosine-
7	1217	71.3	1467	20	AAK25570	Human altered sph
8	401.6	23.5	1746	23	ABLI4565	Drosophila melanog

9	401.6	23.5	1782	23	ABLI4555	Drosophila melanog
10	401.6	23.5	2060	22	AAD06842	Drosophila melanog
11	284.4	16.7	785	20	AAZ06343	Sphingosine-1-phos
12	256.2	15.0	1770	20	AAK25569	Yeast sphingosine-
13	256.2	15.0	2270	22	AAH29742	S. cerevisiae apopt
14	225.6	13.2	1629	20	AAK25568	C. elegans sphingo
15	224.4	13.1	4937	23	ABLI4554	Drosophila melanog
16	224.4	13.1	5187	23	ABLI4564	Drosophila melanog
17	208.2	12.2	1670	21	AAK07526	Fusarium venenatum
18	194.2	11.4	2270	21	AAH29885	C. albicans apoptos
19	182.4	10.7	665	22	AAH08446	Human CDNA clone (
20	182.4	10.7	2955	22	AAH18267	Human CDNA sequenc
21	148	8.7	1092	25	ABK52445	Aspergillus oryzae
22	116.4	6.8	293	21	AAK16916	Human secreted pro
23	72.4	4.2	531	21	AAK40024	Arabidopsis thalia
24	63.8	3.7	349980	22	AAH41225	Pyrococcus abyssi
25	58.4	3.4	60	24	ABN37114	Human spliced tran
26	50.8	3.0	393	22	AAH50937	Lipid degradation
27	50.8	3.0	393	22	AAH56944	P. patens lipid met
28	48.6	2.8	4590	22	AAH24065	Yeast AOD9604-asso
29	39.2	2.3	1830	23	AAH81857	CDNA encoding novel
30	38.2	2.2	2548	25	ABX08975	CDNA encoding huma
31	37.8	2.2	3576	25	ABZ75047	Human kielin-like
32	37.8	2.2	3621	25	ABZ75048	Human kielin-like
33	37.8	2.2	4431	25	ABZ75042	Human kielin-like
34	37.8	2.2	4605	25	ABZ75045	Human kielin-like
35	37.8	2.2	4779	25	ABZ75046	Human kielin-like
36	37.6	2.2	1268	18	AAV74604	Staphylococcus aur
37	37.6	2.2	1835	23	AAH89928	DNA encoding novel
38	37.6	2.2	2503	20	AAK28272	S. aureus p1A cod
39	36.8	2.2	1870	21	AAK33165	Arabidopsis thalia
40	36.2	2.1	293	23	ABV15907	Human prostate exp
41	36.2	2.1	294	23	ABV30204	Human prostate exp
42	36.2	2.1	311	23	ABV45976	Human prostate exp
43	36.2	2.1	471	23	ABV45707	Human prostate exp
44	36.2	2.1	2277	25	ABZ75049	Human kielin-like
45	36.2	2.1	3173	25	ABZ75041	Human kielin-like

ALIGNMENTS

RESULT 1	
AAK25567	
ID	AAK25567 standard; CDNA; 1707 bp.
AC	AAK25567;
XX	
XX	02-AUG-1999 (first entry)
DE	Human sphingosine-1-phosphate lyase CDNA.
XX	
KW	Sphingosine-1-phosphate lyase; SPL; human; breast cancer;
KW	diagnosis; prognosis; therapy; ss.
XX	
OS	Homo sapiens.
PN	W03916888-A2.
XX	
PD	08-APR-1999.
XX	
PF	29-SEP-1998; 98WO-US20365.
XX	
PR	29-SEP-1997; 97US-0939309.
XX	
PA	(CHILD-) CHILDREN'S HOSPITAL OAKLAND RES INST.
PI	Saba JD, Zhou J;
XX	
XX	WPI; 1999-263700/22.
DR	P-PSDB; AAY05827.
XX	
PT	Sphingosine-1-phosphate lyase, polynucleotides and modulators

XX Claim 1: Page 68-72: 96bp; English.

PS This is the nucleotide sequence of human cDNA coding for
CC sphingosine-1-phosphatase (SPL, see AY05827). SPL cDNA was
CC obtained by amplification of human fibroblast RNA. SPL
CC catalyzes the cleavage of sphingosine-1-phosphate into inactive
CC metabolites. Sphingosine-1-phosphate is an endogenous tumour
CC suppressor lipid that potentially inhibits breast cancer cell growth
CC and invasiveness, while not affecting the growth of non-tumour
CC cells. Mouse and human SPL polynucleotides (see AX25666-67) and
CC polypeptides (see AY05826-29) are claimed. Methods are provided for
CC preparing SPL using transformed or transfected host cells. SPL
CC polypeptides are used in claimed methods for identifying agents that
CC modulate SPL activity. SPL inhibitors will inhibit growth of cancer
CC cells, especially breast cancer cells. SPL inhibitors, including
CC polynucleotides preventing expression of SPL genes, or antibodies
CC against SPL, can also be used to prevent the development and/or
CC metastasis of cancer, especially where the inhibitor is linked to
CC an antitumour or antioestrogen receptor antibody. Detection of
CC alterations in an endogenous SPL sequence, especially where the
CC alteration is a deletion of residues 354-433 of the 568 amino acid
CC human SPL sequence (see also AY05830), can be used to diagnose
CC cancer, and to assess the prognosis for recovery.

XX Sequence 1707 BP: 467 A; 388 C; 424 G; 428 T; 0 other;

Query Match 100.0%; Score 1707; DB 20; Length 1707;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTAGACAGACCTTCTGATGTTGAAGCCCTTGAGCCCTACTAGAGATTTTGAA 60
DB 1 ATGCTAGACAGACCTTCTGATGTTGAAGCCCTTGAGCCCTACTAGAGATTTTGAA 60
QY 61 GATATCTCCACAAAGCCAGAAATATGTAATGACATGACCAAGATATAGCCCTGG 120
DB 61 GATATCTCCACAAAGCCAGAAATATGTAATGACATGACCAAGATATAGCCCTGG 120
QY 121 CAGCTAATTTGATGAGTGTCTGTGAGACCCCTGCTGATAGTCTGGGGATATGTTGTC 180
DB 121 CAGCTAATTTGATGAGTGTCTGTGAGACCCCTGCTGATAGTCTGGGGATATGTTGTC 180
QY 181 TTCACGCCAGAGATTTATGTCAGAGTTTAAAAAGAAATGTTTAAAGCTCACAGAG 240
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DB 361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGAGCCCTTCTGG 420
QY 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAACTCACTGAGCTCTT 480
DB 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAACTCACTGAGCTCTT 480
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DB 481 GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGCATCCAGATATCTTCCACAGA 540
QY 541 CTAGCAAGATGAGAGCAAAATTTGTAGAGATAGCTTGTCCCTTTCAATGGGGACCA 600
DB 541 CTAGCAAGATGAGAGCAAAATTTGTAGAGATAGCTTGTCCCTTTCAATGGGGACCA 600
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DB 601 GATTGCTGATGTGTACTTCTGAGGGAACAGAAACATATCATGCTGCTGCAAAACA 660
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DB 841 GCCATGCTGCTATTTAACCCACAGTTTCTCATGCTGTAATAGATCTGTCCCTGAA 900
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DB 1021 GTGAAGGTGTACACGAGATTTACAGCTGACACCCATTAAGTATGCTATGCCCAAAAGC 1080
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DB 1081 TCATCATGCTGCTTATATAGTACAGAAAGTACAGAACTATCACTTCTTGTGATACCA 1140
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DB 1141 GATTGGCAGGGGTGGATCATGCTTCCCAACATCGCAGAGCTCAGGCTGTGATTT 1200
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QY 1381 TACGACATATCAAAACCTGATGACGCTAAGGGGTGAACCTTGAACAGTTCGATTCCTCA 1440
DB 1381 TACGACATATCAAAACCTGATGACGCTAAGGGGTGAACCTTGAACAGTTCGATTCCTCA 1440
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DB 1441 CCCAGTATTCATTTCTGATCAGATTAACAGCCCGGAAACGATGCTATACAAATTC 1500
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DB 1501 CTAAGGACATTCGAGATCTGTCACTCAATCAATCAAGAAATCCATAAGCAAGACCA 1560
QY 1561 GGAATGGGTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 GGAATGGGTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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DB 1621 TTGTCCTAGTCTTTTGGAGAGCTTGTACAGCAACCCAGTACACCCAGGAGCCAG 1680
QY 1681 ATGAATGGTCTTCCAAACCCCACTGA 1707
DB 1681 ATGAATGGTCTTCCAAACCCCACTGA 1707

RESULT 2
ABL59529

ID	ABL59529	standard;	CDNA;	1707	BP.
XY					

AC ABL59529;

DT 16-JUL-2002 (first entry)

	Human sphingosine-1-phosphate lyase 1	CDNA SEQ ID NO:29.
DE		
XY		

Human; sphingosine-1-phosphate lyase 1; enzyme;
 KM
 KM
 Tumour; lipid associated gene; lipid metabolism;
 KM

chromosome 10q21; gene, ss.

OS Homo sapiens.
XX

PN WO200227028-A

PD 04-APR-2002.

XX 27-SEP-2001; 2001WO-US30366.
PF

XX 28-SEP-2000. 2000RS-0676052
PR

XX
XX

PA (AVAL-) AVALRGIN TECHNOLOGIES INC.
XX

PI	Skinner MK, Patton JL, Chaudhary J;
XX	

DR WPI; 2002-402054/43.
XX

PT Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action -
xy

Example 1; Page 87; 113pp; English.

The present invention describes a method for identifying tumour characteristics, comprising measuring a copy number or expression level of at least two genes associated with lipid metabolism, synthesis, or action in cells from a patient tissue sample, and comparing the results with a copy number or expression level of the genes in a normal cell. Also described is an array of nucleic acid polymers immobilised on a solid support, comprising a solid support, at least two different nucleic acid polymers which are each specific for a different gene associated with lipid metabolism, synthesis or action, where each nucleic acid polymer is located at a predetermined position on the solid support, and the array comprises nucleic acid polymers which are specific for less than 100 genes other than the selected genes. The method is useful for determining tumour characteristics in a tissue sample taken from a patient. The present sequence represents a human lipid-associated gene related cDNA sequence, which is used in the exemplification of the present invention.

aa Sequence 1707 BP; 468 A; 386 C; 425 G; 428 T; 0 other

Query Match	99.7%	Score 1702.2	DB 24	Length 1707
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1704; Conservative	0	Mismatches	3	Indels 0; Gaps 0

QY 1 ATGCCATGACAGACCTTCTGATGTTGAAGCCCTTTAGGCCCTACTTAAGAGATTTTGGAA 60

Db 1 ATGCCATGACAGACCTTCTGATGTTGAAGCCCTTTAGGCCCTACTTAAGAGATTTTGGAA 60

QY 61 GTATTACTCCACAAAAGCCAGAATTAATGTAATGAGACTTGACACCAAGTATGAGCCCTGG 120

Db 61 GTATTACTCCACAAAAGCCAGAATTAATGTAATGAGACTTGACACCAAGTATGAGCCCTGG 120

QY 121 CAGCTAATTGCATGAGATGTCGCTGCGAGACCCCTGCGGATAGCTGCGGGATATGAGTTTGTG 180

Db 121 CAGCTAATTGCATGAGATGTCGCTGCGAGACCCCTGCGGATAGCTGCGGGATATGAGTTTGTG 180

QY 121 CAGCTAATTGCATGAGATGTCGCTGCGAGACCCCTGCGGATAGCTGCGGGATATGAGTTTGTG 180

Db 121 CAGCTAATTGCATGAGATGTCGCTGCGAGACCCCTGCGGATAGCTGCGGGATATGAGTTTGTG 180

OY	181	TTCCAGCCGAGAGAGTTTATGGTCMAAGGTTTAAAGAAATGTTTAAAGTCACCGAGAA	240
Dp	181	TTCCAGCCGAGAGAGTTTATGGTCMAAGGTTTAAAGAAATGTTTAAAGTCACCGAGAA	240
OY	241	ATGCCCATATATTGGTCTGTAGATTCAACACAAAGTTGAACACAGACCAGGATATATTAGC	300
Dp	241	ATGCCCATATATTGGTCTGTAGATTCAACACAAAGTTGAACACAGACCAGGATATATTAGC	300
OY	301	AAGAACATGTCATTCTGAAAAGTGACAAAGAGTATGTGAAAGCTTTTACCCTCCAGGGT	360
Dp	301	AAGAACATGTCATTCTGAAAAGTGACAAAGAGTATGTGAAAGCTTTTACCCTCCAGGGT	360
OY	361	CTGAGCCTATCTGCTGTTTGGAGAAACTTAAAGAGTACAGCTCATAGAGCCCTTCTGG	420
Dp	361	CTGAGCCTATCTGCTGTTTGGAGAAACTTAAAGAGTACAGCTCATAGAGCCCTTCTGG	420
OY	421	CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAACCTCAGTACGCTCTT	480
Dp	421	CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAACCTCAGTACGCTCTT	480
OY	481	GTGAAGGCTTATGAGAGATTTTTCATGAGATTAACCCCTGCAATCCAGATATCTTCCACAGA	540
Dp	481	GTGAAGGCTTATGAGAGATTTTTCATGAGATTAACCCCTGCAATCCAGATATCTTCCACAGA	540
OY	541	CTACGCAAGATATAGAGCGCAAAATTTGTAGAGTACGTTTCTCCCTGTTCAATGGGGACCA	600
Dp	541	CTACGCAAGATATAGAGCGCAAAATTTGTAGAGTACGTTTCTCCCTGTTCAATGGGGACCA	600
OY	601	GATTCGTTGATGTGATCTTCTGGGGGAGACAGAAACATACATGAGCCCTGCACAAAGCA	660
Dp	601	GATTCGTTGATGTGATCTTCTGGGGGAGACAGAAACATACATGAGCCCTGCACAAAGCA	660
OY	661	TGTGCGGATCTGGCCCTTTGAGAAAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
Dp	661	TATGCGGATCTGGCCCTTTGAGAAAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
OY	721	GCCCATGCTGCATTTAACAAAGACGCCAGTTACTTTGGGATGTAATTTGTGGGGTCCCA	780
Dp	721	GCCCATGCTGCATTTAACAAAGACGCCAGTTACTTTGGGATGTAATTTGTGGGGTCCCA	780
OY	781	TTGACGAAGATATGAGAGTGGATGTGAGGCAATGAGAAAGCATATCTCCAGAAACT	840
Dp	781	TTGACGAAGATATGAGAGTGGATGTGAGGCAATGAGAAAGCATATCTCCAGAAACT	840
OY	841	GCCATGCTGCTGTTCTTACCCCAACAGTTTCCCTCATGGTGTAAATAGATCTTGTCCCTGAA	900
Dp	841	GCCATGCTGCTGTTCTTACCCCAACAGTTTCCCTCATGGTGTAAATAGATCTTGTCCCTGAA	900
OY	901	GTGGCCAAAGCTGGCTGTCAATACAAATACCCTTCATGTTCGACAGCTTTGTGGGAGGC	960
Dp	901	GTGGCCAAAGCTGGCTGTCAATACAAATACCCTTCATGTTCGACAGCTTTGTGGGAGGC	960
OY	961	TTCTCTCATCTGCTTATGAGAAAGACAGATATACCCTGAGACACCATTGATTTCCGG	1020
Dp	961	TTCTCTCATCTGCTTATGAGAAAGACAGATATACCCTGAGACACCATTGATTTCCGG	1020
OY	1021	GTGAAGGTGTAAACCAGCATTTACAGCTGACACCCTAAGTATGGTATGCCCAAAAGGC	1080
Dp	1021	GTGAAGGTGTAAACCAGCATTTACAGCTGACACCCTAAGTATGGTATGCCCAAAAGGC	1080
OY	1081	TCATCATTTGGTGTGTATATAGTACAAAGATATACAGAACTATCACTTTCTTGGTGCATACA	1144
Dp	1081	TCATCATTTGGTGTGTATATAGTACAAAGATATACAGAACTATCACTTTCTTGGTGCATACA	1144
OY	1141	GATTGGCAGGTGGCATATATGCTTTCCCAACATCGAGAGCTCACGGCTCTGTTGGGCATT	1200
Dp	1141	GATTGGCAGGTGGCATATATGCTTTCCCAACATCGAGAGCTCACGGCTCTGTTGGGCATT	1200
OY	1201	AGCCGAGCCTGTGGGCTGCTTATGATGACCTTTCGGTGAAGACGGCTATGTTGAAGCTAC	1260
Dp	1201	AGCCGAGCCTGTGGGCTGCTTATGATGACCTTTCGGTGAAGACGGCTATGTTGAAGCTAC	1260
OY	1261	AAACAGATCATCAAAACTGCTGCGCTTCTCTCAAGTCAGACATGGAATAATATCAAAAGCATC	1320
Dp	1261	AAACAGATCATCAAAACTGCTGCGCTTCTCTCAAGTCAGACATGGAATAATATCAAAAGCATC	1320

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DB      1261 AATGATATATCAAAAGTCTGCTTCTCAAGTCAAGAACTGGAATATCAAAAGGATC 1320
QY      1321 TTTGTTTTGGGAATCCCAATTTGTCATCTGCTGGATCCGATATTTTGACATC 1380
DB      1321 TTTGTTTTGGGAATCCCAATTTGTCATCTGCTGGATCCGATATTTTGACATC 1380
QY      1381 TACCGATCTCAAACTGATGACTGCTAAGGGGTGAGACTTGAACCAAGTTGACATTC 1440
DB      1381 TACCGATCTCAAACTGATGACTGCTAAGGGGTGAGACTTGAACCAAGTTGACATTC 1440
QY      1441 CCCAGATTCATTTTGGCATCTACATCAACGCCCCGAAACGATCTATACATTC 1500
DB      1441 CCCAGATTCATTTTGGCATCTACATCAACGCCCCGAAACGATCTATACATTC 1500
QY      1501 CTAAAGGACATTCGAGAAATCTGCTCAATCATGAAGATCTTAAAGCAAGACCA 1560
DB      1501 CTAAAGGACATTCGAGAAATCTGCTCAATCATGAAGATCTTAAAGCAAGACCA 1560
QY      1561 GGAATGGGTGCATCTATGCTGACGAGCACTGTTGACAGAAATGTTGTCAGAA 1620
DB      1561 GGAATGGGTGCATCTATGCTGACGAGCACTGTTGACAGAAATGTTGTCAGAA 1620
QY      1621 TTGCTCTAGTCTTCTTGAGACGCTTGTACAGACGACCTGACCCAGGGGAGCCAG 1680
DB      1621 TTGCTCTAGTCTTCTTGAGACGCTTGTACAGACGACCTGACCCAGGGGAGCCAG 1680
QY      1681 ATGAATGTTCTTCCAAACCCCACTGA 1707
DB      1681 ATGAATGTTCTTCCAAACCCCACTGA 1707

RESULT 3
AA206342
ID      AA206342 standard; DNA; 2130 BP.
XX
AC      AA206342;
XX
DT      26-OCT-1999 (first entry)
XX
DE      Sphingosine-1-phosphate lyase nucleotide sequence.
XX
KM      sphingosine-1-phosphate; sphingosine-1-phosphate lyase; SPHINGLY;
KM      G-protein coupled receptor; EDS-1; secondary messenger; cancer;
KM      cardiovascular disorder; thrombosis; atherosclerosis; wound healing;
KM      stroke; apoptosis; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      178..1384
FT      FT      /tag= a
FT      FT      /product= "Sphingosine-1-phosphate lyase"
XX
PN      WO938983-A1.
XX
PD      05-AUG-1999.
XX
PF      24-DEC-1998; 98MO-EP08564.
XX
PR      03-NOV-1998; 98GB-0024026.
PR      29-JAN-1998; 98EP-0300625.
XX
XX      (SMK ) SMITHKLINE BEECHAM PLC.
XX
XX      Duckworth DM, Godden RJ, Testa TT;
XX
XX      WPI: 1999-479192/40.
XX      P-PSDB: AA15211.
XX
XX      A new sphingosine-1 phosphate lyase useful for diagnosing and
XX      treating cancers, cardiovascular disorders, thrombosis or
XX      atherosclerosis
XX

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XX      Claim 7; Page 23; 37pp; English.
PS
XX      This is the nucleotide sequence of Sphingosine-1-phosphate lyase. The
CC      lyase catalyses the cleavage of Sphingosine-1-phosphate to give a long
CC      chain aldehyde and phosphoethanolamine.
CC      The sequence can form the basis of a method of treating cancers, cardiac
CC      disorders, thrombosis, atherosclerosis and other conditions. This is due
CC      to the action of sphingosine-1-phosphate intracellularly as a secondary
CC      messenger and extracellularly as a ligand for the G-protein coupled
CC      receptor EDG-1.
XX
XX      Sequence 2130 BP; 563 A; 479 C; 561 G; 527 T; 0 other:
SQ
Query Match      99.5%; Score 1699; DB 20; Length 2130;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY      1 ATGCTAGCAGACACCTTGTATGTTGAAGCCCTTGAGCCCTACTAGATTTTGGAA 60
DB      178 ATGCTAGCAGACACCTTGTATGTTGAAGCCCTTGAGCCCTACTAGATTTTGGAA 237
QY      61 GATATCTCCAAAGGCCAAGAAATTAATGAAATGGACATTTGACCAAGATAGCCCTGG 120
DB      238 GATATCTCCAAAGGCCAAGAAATTAATGAAATGGACATTTGACCAAGATAGCCCTGG 297
QY      121 CAGCTAATTGCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGATTTGTC 180
DB      298 CAGCTAATTGCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGATTTGTC 357
QY      181 TTCCAGCCAGAGAGTTTATGTCAAAGTTTAAAAAGAAATGTTTAACTACACAGANG 240
DB      358 TTCCAGCCAGAGAGTTTATGTCAAAGTTTAAAAAGAAATGTTTAACTACACAGANG 417
QY      241 ATGCCCATATTTGTCGTATGATCAAGCAAGTGAACCAAGCAAGCAAGATATTTTGGC 300
DB      418 ATGCCCATATTTGTCGTATGATCAAGCAAGTGAACCAAGCAAGCAAGATATTTTGGC 477
QY      301 AAGAACATGTCATCTCTGTAAGTGAACAAGATATGTAAGTAAAGCTTACCTCCAGGGT 360
DB      478 AAGAACATGTCATCTCTGTAAGTGAACAAGATATGTAAGTAAAGCTTACCTCCAGGGT 537
QY      361 CTGAGCTATCTGCTGTTTGGAGAACTTAAGAGATACAGTCTATAGGAGCCCTTGG 420
DB      538 CTGAGCTATCTGCTGTTTGGAGAACTTAAGAGATACAGTCTATAGGAGCCCTTGG 597
QY      421 CAAGAGGGAGAGCCCTGGAACAGTACAGTGGGAGAGAGAACTCACTAGCTCCTT 480
DB      598 CAAGAGGGAGAGCCCTGGAACAGTACAGTGGGAGAGAGAACTCACTAGCTCCTT 657
QY      481 GTGAAGGCTTATGAGATTTTGCATGAGATAACCCCTGCAATCAAGATATCTTCCAGGA 540
DB      658 GTGAAGGCTTATGAGATTTTGCATGAGATAACCCCTGCAATCAAGATATCTTCCAGGA 717
QY      541 CTAGCAAGATGAGAGCAAGAAATGAGATAGCTTGTCCCTTCAATGGGGAGACA 600
DB      718 CTAGCAAGATGAGAGCAAGAAATGAGATAGCTTGTCCCTTCAATGGGGAGACA 777
QY      601 GATTGCTGATGATGTCATCTTGGGGAAACAGAAACATATCTAGGCTGCAAAACA 660
DB      778 GATTGCTGATGATGTCATCTTGGGGAAACAGAAACATATCTAGGCTGCAAAACA 837
QY      661 TGTGGGATCTGGCCCTTGGAGAGGGATCAAAACTCCAGAAATTTGGCTCCCAANGT 720
DB      838 TATCGGATCTGGCCCTTGGAGAGGGATCAAAACTCCAGAAATTTGGCTCCCAANGT 897
QY      721 GCCCATGCTGATTTAAACAAGCAGCACTTACTTTGGAGTAAGATTTGGGGTCCCA 780
DB      898 GCCCATGCTGATTTAAACAAGCAGCACTTACTTTGGAGTAAGATTTGGGGTCCCA 957
QY      781 TTGACGAAGATGATGAGGTGATGTGAGGCAATGAAAGCATATCTCCAGAAACT 840
DB      958 TTGACGAAGATGATGAGGTGATGTGAGGCAATGAAAGCATATCTCCAGAAACT 1017

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QY 841 GCCATGCTGCTGTTCTTCTACCCACAGTTTCTCATGATGTATAGATCTGTCCTGAA 900
   |||||||
DB 1018 GCCATGCTGCTGTTCTTCTACCCACAGTTTCTCATGATGTATAGATCTGTCCTGAA 1077
QY 901 GTGGCCAAAGCTGGCTGCAAAATACAAATACCCCTTCATGTCGACGCTTGTGGAAGC 960
   |||||||
DB 1078 GTGGCCAAAGCTGGCTGCAAAATACAAATACCCCTTCATGTCGACGCTTGTGGAAGC 1137
QY 961 TTCCCTATGCTCTTTTATGGAAGACAGATACCCACTGAGACACCATTTGATTTCCGG 1020
   |||||||
DB 1138 TTCCCTATGCTCTTTTATGGAAGACAGATACCCACTGAGACACCATTTGATTTCCGG 1197
QY 1021 GTGAAGGTGTACACGACATTTGACGTGACACGACATTAAGTATGCTATGCCCCAAAAAGC 1080
   |||||||
DB 1198 GTGAAGGTGTACACGACATTTGACGTGACACGACATTAAGTATGCTATGCCCCAAAAAGC 1257
QY 1081 TCATCATTTGGTGTGTTATAGTACAAAGAGTACAGAACTATGATTTCTTCGTGATACA 1140
   |||||||
DB 1258 TCATCATTTGGTGTGTTATAGTACAAAGAGTACAGAACTATGATTTCTTCGTGATACA 1317
QY 1141 GATTGCGAGGCTGTCATCTATGCTTCCCAACCATGCGACGCTCAGGCTGTGTCATT 1200
   |||||||
DB 1318 GATTGCGAGGCTGTCATCTATGCTTCCCAACCATGCGACGCTCAGGCTGTGTCATT 1377
QY 1201 AGGCGACGCTGTTGGGCTGCTGATGACATTTGGGTGAGAAAGGCTATGTTGAAGCTACC 1260
   |||||||
DB 1378 AGGCGACGCTGTTGGGCTGCTGATGACATTTGGGTGAGAAAGGCTATGTTGAAGCTACC 1437
QY 1261 AAGCAGATCATCAAAACTGCTGCTTCCTCCTCAGTCAAGTCAAGAAATATCAAAAGCATC 1320
   |||||||
DB 1438 AAGCAGATCATCAAAACTGCTGCTTCCTCCTCAGTCAAGTCAAGAAATATCAAAAGCATC 1497
QY 1321 TTGTTTGGGGAATCCCAATGTCATCTATGCTGTCGATCCGTCATTTTGACATC 1380
   |||||||
DB 1498 TTGTTTGGGGAATCCCAATGTCATCTATGCTGTCGATCCGTCATTTTGACATC 1557
QY 1381 TACCGCATCATCAAACTGATGACTGCTAAGGGGTGAAAGTGAACGATGTCAGTTCCCA 1440
   |||||||
DB 1558 TACCGCATCATCAAACTGATGACTGCTAAGGGGTGAAAGTGAACGATGTCAGTTCCCA 1617
QY 1441 CCCAGTATTCATTTGTCATCACATTAACACGCGCGGAAGAGTATGATACATTC 1500
   |||||||
DB 1618 CCCAGTATTCATTTGTCATCACATTAACACGCGCGGAAGAGTATGATACATTC 1677
QY 1501 CTTAAGGACATTTGAGAGATGTCACCTCAATCATGAAGATCTTAAGCGAAGACCACA 1560
   |||||||
DB 1678 CTTAAGGACATTTGAGAGATGTCACCTCAATCATGAAGATCTTAAGCGAAGACCACA 1737
QY 1561 GGAATGGGTGCCATCTATGCGCATGGCCGACAGACAAGTGTGAAGAAATATGTTGCGAA 1620
   |||||||
DB 1738 GGAATGGGTGCCATCTATGCGCATGGCCGACAGACAAGTGTGAAGAAATATGTTGCGAA 1797
QY 1621 TTGTCCTCATGCTTTCTTGGACAGCTGTGACAGCAGCAGACTGTCAACCCAGGACGACG 1680
   |||||||
DB 1798 TTGTCCTCATGCTTTCTTGGACAGCTGTGACAGCAGCAGCTGTCAACCCAGGACGACG 1657
QY 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
   |||||||
DB 1858 ATGAATGTTCTCCAAAACCCCACTGA 1884

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RESULT 4
AAK51594
ID AAK51594 standard; cdna: 2446 BP.

AC AAK51594;

DT 06-NOV-2001 (first entry)

DE Human polynucleotide SEQ ID NO 139.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

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KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
OS Homo sapiens.
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
DR WPI: 2001-476283/51.
DR P-PSDB: AAM78461.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
PS
PS Claim 1; Page 825-827; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 2446 BP; 625 A; 541 C; 621 G; 657 T; 2 other:
Query Match 99.5%; Score 1699; DB 22; Length 2446;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGCCCTATGACACAGCTTTCGATGTTGAAGCCCTTGAAGCCCTTATAGATTTTGAA 60
   |||||||
DB 200 ATGCCCTATGACACAGCTTTCGATGTTGAAGCCCTTGAAGCCCTTATAGATTTTGAA 259
QY 61 GTATATCTCCACAAAGCCAGCAATTAATGATGACATTGACCAAGTATGAGCCCTGG 120
   |||||||
DB 260 GTATATCTCCACAAAGCCAGCAATTAATGATGACATTGACCAAGTATGAGCCCTGG 319
QY 121 CAGCTAATTCATGAGTGTGCTGTGACCCCTGCTGATGCTGGGATATGAGTTTGTG 180
   |||||||
DB 320 CAGCTAATTCATGAGTGTGCTGTGACCCCTGCTGATGCTGGGATATGAGTTTGTG 379
QY 181 TTCGAGCAGAGAGTTTATGCTCAAGTTTAAAAAGAAAGTTTAAAGCTCACAGAGAAG 240
   |||||||
DB 380 TTCGAGCAGAGAGTTTATGCTCAAGTTTAAAAAGAAAGTTTAAAGCTCACAGAGAAG 439
QY 241 ATGCCCATTTATGCTGTAAGATTCAAGACAAGTTGAACAAGCAAGATGATATTAGC 300

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440 ATGCCATTTATTTGGTGTGAAGATTCAAGCAAGTTGAACAAACCAAGATATATATTAC 499
OY 301 AAGAACATGTCAATTCCTGAAAGTGCACAAAGATATGTAAAGCTTTACCTCCAGGT 360
Db 500 AAGAACATGTCAATTCCTGAAAGTGCACAAAGATATGTAAAGCTTTACCTCCAGGT 559
OY 361 CTGAGCTCATCTGCTGTGTTTGGAGAACTTAAAGATACAGCTCTATGGAGCCCTTCTGG 420
Db 560 CTGAGCTCATCTGCTGTGTTTGGAGAACTTAAAGATACAGCTCTATGGAGCCCTTCTGG 619
OY 421 CAAGAGGGAGAGCCCTGGAAGTGTACAGTGTGAGGAGAGAGAGTCACTAGCTCCTT 480
Db 620 CAAGAGGGAGAGCCCTGGAAGTGTACAGTGTGAGGAGAGAGTCACTAGCTCCTT 679
OY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAGATATCTTCCAGGA 540
Db 680 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAGATATCTTCCAGGA 739
OY 541 CTACGCAGATATGAGGAGCAAAATTTGTAGAGATAGCTTGTCCCTGTTCAATGGGGACCA 600
Db 740 CTACGCAGATATGAGGAGCAAAATTTGTAGAGATAGCTTGTCCCTGTTCAATGGGGACCA 799
OY 601 GATTGCTGTGATGTGTGACTTCTGGGGGACAGAAAGCATCTCATGAGCCCTGCAAAAGA 660
Db 800 GATTGCTGTGATGTGTGACTTCTGGGGGACAGAAAGCATCTCATGAGCCCTGCAAAAGA 859
OY 661 TGTGGGGATCTGGCCCTTGTGAGAGGGGATCAAAAGCTCCAGAAATTTGGGCTCCCAAGT 720
Db 860 TATCGGGATCTGGCCCTTGTGAGAGGGGATCAAAAGCTCCAGAAATTTGGGCTCCCAAGT 919
OY 721 GCCCATGCTGCAATTTAACAAAGCAGCCAGTTACTTTGGATGAAGATTTGGGGTCCCA 780
Db 920 GCCCATGCTGCAATTTAACAAAGCAGCCAGTTACTTTGGATGAAGATTTGGGGTCCCA 979
OY 781 TTGACGAAGATATGAGAGTGTGAGGGCAATGAGAGAGTATCTCCAGGAACACT 840
Db 980 TTGACGAAGATATGAGAGTGTGAGGGCAATGAGAGAGTATCTCCAGGAACACT 1039
OY 841 GCCATGCTGCTGTGTTCTAACCCACAGTTTCTCTCATGTGTAAATGATCTGCTCCGTA 900
Db 1040 GCCATGCTGCTGTGTTCTAACCCACAGTTTCTCTCATGTGTAAATGATCTGCTCCGTA 1099
OY 901 GTGGCCAGCTGCTGTCAATAATCAAAATACCCCTTCATGTGAGCGCTTGTGGAGGC 960
Db 1100 GTGGCCAGCTGCTGTCAATAATCAAAATACCCCTTCATGTGAGCGCTTGTGGAGGC 1159
OY 961 TTCTCATGCTCTTATGAGAGAAAGCAGATACCCACAGGAGCAGCCCATTTGATTTCCGG 1020
Db 1160 TTCTCATGCTCTTATGAGAGAAAGCAGATACCCACAGGAGCAGCCCATTTGATTTCCGG 1219
OY 1021 GTGAAGGTGTAAACAGCATTTACGCTGACACCCATTAATGCTATGCCCAAAAGC 1080
Db 1220 GTGAAGGTGTAAACAGCATTTACGCTGACACCCATTAATGCTATGCCCAAAAGC 1279
OY 1081 TCATCATGTGTGTATATAGTACAGAAAGTACAGAACTATCACTTCTGTCATACA 1140
Db 1280 TCATCATGTGTGTATATAGTACAGAAAGTACAGAACTATCACTTCTGTCATACA 1339
OY 1141 GATTGGCAGGAGTGTATGCTTCCCAACATCGGAGGCTACGGCTGTGGGCAAT 1200
Db 1340 GATTGGCAGGAGTGTATGCTTCCCAACATCGGAGGCTACGGCTGTGGGCAAT 1399
OY 1201 AGCGAGGCTGTGGGCTGCCCTTGATGACATTCGGTGAAGCGCTATGTTGAAGCTACC 1260
Db 1400 AGCGAGGCTGTGGGCTGCCCTTGATGACATTCGGTGAAGCGCTATGTTGAAGCTACC 1459
OY 1261 AAACGATCATCAAAAGCTGCTGCTCTCAAGTACAGAACTGGAATAATCAAGGCAATC 1320
Db 1460 AAACGATCATCAAAAGCTGCTGCTCTCAAGTACAGAACTGGAATAATCAAGGCAATC 1519
OY 1321 TTTGTTTTGGGAATCCCAATTTGTCATCAATGCTCGGGATCCCGGATTTTGACATC 1380
|||||

Db 1520 TTTGTTTTGGGAATCCCAATTTGTCATCAATGCTCTGCGGATCCCGTATTTTGACATC 1579
OY 1381 TACCGCATATCAAAACCTGATGACTGCTAAGGGGTGGAACCTTAACCACTTGCAGTCCCA 1440
Db 1580 TACCGCATATCAAAACCTGATGACTGCTAAGGGGTGGAACCTTAACCACTTGCAGTCCCA 1639
OY 1441 CCCAGTATTCATTTCTGATCAATTAACACGCCCGGAAGAGTACTATACATTC 1500
Db 1640 CCCAGTATTCATTTCTGATCAATTAACACGCCCGGAAGAGTACTATACATTC 1699
OY 1501 CTAAAGGACATTCGGAATCTGCACTCAATCAATGAAGAAATCTAAAGCGAAGCCCA 1560
Db 1700 CTAAAGGACATTCGGAATCTGCACTCAATCAATGAAGAAATCTAAAGCGAAGCCCA 1759
OY 1561 GGAATGGGTGCCATCATATGATGCCAGCCAGACAGCTGTGACAGGAATATGTTGCAGAA 1620
Db 1760 GGAATGGGTGCCATCATATGATGCCAGCCAGACAGCTGTGACAGGAATATGTTGCAGAA 1819
OY 1621 TTTGCTCAGTCTTCTTGGACAGCTTTGACACAGCCAGACCTGTACCCAGGACCCAG 1680
Db 1820 TTTGCTCAGTCTTCTTGGACAGCTTTGACACAGCCAGACCTGTACCCAGGACCCAG 1879
OY 1681 ATGAATGGTTCCTCAAAACCCCACTGA 1707
Db 1880 ATGAATGGTTCCTCAAAACCCCACTGA 1906

RESULT 5

AAK52578
ID AAK52578 standard; cDNA; 2093 BP.

AAK52578;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 2107.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PE 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

PA (HSE-) HSEQ INC.

Tang YT, Liu C, Dimaenac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;

WPI: 2001-476283/51.
P-PSDB: AAM79445.

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -

Claim 1; Page 4485; 6221pp; English.

CC The invention relates to polynucleotides (AA51456-AA53435) and the
CC encoded polypeptides (AA87823-AA80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC (Note: Records for SEQ ID NO 2110 (AA52581), 2111 (AA52582) and 3666
CC (AA80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.)

XX Sequence 2093 BP; 565 A; 465 C; 539 G; 524 T; 0 other;

Query Match 99.4%; Score 1697.4; DB 22; Length 2093;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1701; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGCCTAGCAGACCTTCTGATGTTGAAGCCCTTGAGCCCTACTTAAGATTTTGAA 60
DB 133 ATGCCTAGCAGACCTTCTGATGTTGAAGCCCTTGAGCCCTACTTAAGATTTTGAA 192
QY 61 GATATCTCCAAAACCAAGAAATTAATGAGCATTTGACCAAGATATGAGCCCTG 120
DB 193 GATATCTCCAAAACCAAGAAATTAATGAGCATTTGACCAAGATATGAGCCCTG 252
QY 121 CAGCTAATTCATGAGTGTCTGTGACCTGCTGTAAGTCTGAGGATATGAGTTGTC 180
DB 253 CAGCTAATTCATGAGTGTCTGTGACCTGCTGTAAGTCTGAGGATATGAGTTGTC 312
QY 181 TTCCAGCCAGAGATTATGCTCAAGTTTAAAAAATGTTTAAGCTCAGCAGAGAG 240
DB 313 TTCCAGCCAGAGATTATGCTCAAGTTTAAAAAATGTTTAAGCTCAGCAGAGAG 372
QY 241 ATGCCATTATTGCTGCTGAAGATTCAAGCAAGTTGAACAGCAAGATGATATTAGC 300
DB 373 ATGCCATTATTGCTGCTGAAGATTCAAGCAAGTTGAACAGCAAGATGATATTAGC 432
QY 301 AAGAACATGTCATCTCTGAAAGTGAGCAAAAGATATGTAAAGCTTACCTCCAGGGT 360
DB 433 AAGAACATGTCATCTCTGAAAGTGAGCAAAAGATATGTAAAGCTTACCTCCAGGGT 492
QY 361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGAGCCCTTCTG 420
DB 493 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGAGCCCTTCTG 552
QY 421 CAAGAGGGAGAGCCCTCTGGAACAGTGAAGTGGGGAGAGAAAGCTCACTGAGCTCT 480
DB 553 CAAGAGGGAGAGCCCTCTGGAACAGTGAAGTGGGGAGAGAAAGCTCACTGAGCTCT 612
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAGATATCTTCCAGGA 540
DB 613 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAGATATCTTCCAGGA 672
QY 541 CTACGCAATATAGAGCAGAAATTTGAGAGTATGCTTCTCTCAATGGGGAGCA 600
DB 673 CTACGCAATATAGAGCAGAAATTTGAGAGTATGCTTCTCTCAATGGGGAGCA 732
QY 601 GATTCTGTGATGATGCTTCTGAGCTTCTGGGGAACAGAAAGCATCTCATGGGCTCCAAAGCA 660
DB 733 GATTCTGTGATGATGCTTCTGAGCTTCTGGGGAACAGAAAGCATCTCATGGGCTCCAAAGCA 792
QY 661 TGTGGGATCTGGCCCTTTGAGAAAGGGATCAAAATCTCAGAAATTTGCTGCCCAAAGT 720
DB 793 TATCGGATCTGGCCCTTTGAGAAAGGGATCAAAATCTCAGAAATTTGCTGCCCAAAGT 852
QY 721 GCCCATGCTGATTTTAAACAAGCAGCTACTTTGGGATGAAGATTTGGCGGTTCCCA 780
DB 853 GCCCATGCTGATTTTAAACAAGCAGCTACTTTGGGATGAAGATTTGGCGGTTCCCA 912
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QY 781 TTGACGAAGATGATGAGGTGATGATGAGGCAATGAGAAGACATCTTCCAGAAACAT 840
DB 913 TTGACGAAGATGATGAGGTGATGATGAGGCAATGAGAAGACATCTTCCAGAAACAT 972
QY 841 GCCATGCTGCTGTTCTTACCCACAGTTTCTCATGATGATGTAATAGATCTGTCCTGAA 900
DB 973 GCCATGCTGCTGTTCTTACCCACAGTTTCTCATGATGATGTAATAGATCTGTCCTGAA 1032
QY 901 GTGGCCCAAGCTGGCTGTCAAAATCAAAATTAACCCCTTCATGTCGACGCTTGTGGAGGC 960
DB 1033 GTGGCCCAAGCTGGCTGTCAAAATCAAAATTAACCCCTTCATGTCGACGCTTGTGGAGGC 1092
QY 961 TTCCCATGCTCTTTATGGAAGAGAGATATCCACTGAGCAGCCATTTGATTTCCGG 1020
DB 1093 TTCCCATGCTCTTTATGGAAGAGAGATATCCACTGAGCAGCCATTTGATTTCCGG 1152
QY 1021 GTGAAGGTTGAACAGATTTTCAAGCTGACACCCATTAATGATGCTATGCCCCAAAGGC 1080
DB 1153 GTGAAGGTTGAACAGATTTTCAAGCTGACACCCATTAATGATGCTATGCCCCAAAGGC 1212
QY 1081 TCATCATTTGCTGTTGATAGTGACAAAGATACAGAACTATAGATTCTTCTGATACA 1140
DB 1213 TCATCATTTGCTGTTGATAGTGACAAAGATACAGAACTATAGATTCTTCTGATACA 1272
QY 1141 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGACAGGCTCACGGCTGGTGCCATT 1200
DB 1273 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGACAGGCTCACGGCTGGTGCCATT 1332
QY 1201 AGCGACGCTGTTGGGCTGCTTGATGACATTCGGTGAGACGGCTATGTTGAAGTACC 1260
DB 1333 AGCGACGCTGTTGGGCTGCTTGATGACATTCGGTGAGACGGCTATGTTGAAGTACC 1392
QY 1261 AAGCAGATCATCAAAACTGCTGCTTCCCAATGCAAGAACTGGAATATCAAAAGCATC 1320
DB 1393 AAGCAGATCATCAAAACTGCTGCTTCCCAATGCAAGAACTGGAATATCAAAAGCATC 1452
QY 1321 TTTGTTTGGGAATCCCAATTTGTCATCTATGCTCTGGGATCCCGTGAATTTTGACATC 1380
DB 1453 TTTGTTTGGGAATCCCAATTTGTCATCTATGCTCTGGGATCCCGTGAATTTTGACATC 1512
QY 1381 TACCGACTATCAAACTGATGACTGCTAAGGGGTGAACTTGAACAGATTTGCCATGCCA 1440
DB 1513 TACCGACTATCAAACTGATGACTGCTAAGGGGTGAACTTGAACAGATTTGCCATGCCA 1572
QY 1441 CCCAGTATCATTTTTCGATCATCATATACAGCCCGGAAAGAGATGATATACAAATTC 1500
DB 1573 CCCAGTATCATTTTTCGATCATCATATACAGCCCGGAAAGAGATGATATACAAATTC 1632
QY 1501 CTAAAGGACATTCGAAATCTGTCACTCAATCATGAAGAATCTTAAAGGAGAGACACA 1560
DB 1633 CTAAAGGACATTCGAAATCTGTCACTCAATCATGAAGAATCTTAAAGGAGAGACACA 1692
QY 1561 GGAATGGTGCATCTATGCCATGAGCCAGACACAATGTTGACAGAAATATGTTGCAGAA 1620
DB 1693 GGAATGGTGCATCTATGCCATGAGCCAGACACAATGTTGACAGAAATATGTTGCAGAA 1752
QY 1621 TTGTCCTCATGCTCTTCTTGGACAGCTGTACAGACCGACATGCAACCCAGGCGAGCAG 1680
DB 1753 TTGTCCTCATGCTCTTCTTGGACAGCTGTACAGACCGACATGCAACCCAGGCGAGCAG 1812
QY 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
DB 1813 ATGAATGTTCTCCAAAACCCCACTGA 1839
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RESULT 6
AA525566
ID AAX25566 standard; cDNA; 1707 BP.
XX AAX25566;
AC
XX
XX 02-AUG-1999 (first entry)
XX

DE	Mouse sphingosine-1-phosphate lyase cDNA.
XX	Sphingosine-1-phosphate lyase; SPL; mouse; breast cancer;
KW	diagnosis; prognosis; therapy; ss.
XX	Mus musculus.
XX	WO9916888-A2.
PM	08-APR-1999.
PD	29-SEP-1998; 98MO-US20365.
PF	29-SEP-1997; 97US-0939309.
PR	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
PA	Saba JD, Zhou J;
PI	WPL: 1999-263700/22.
DR	P-PADB: AAY05826.
XX	Sphingosine-1-phosphate lyase, polynucleotides and modulators
PT	Claim 1; Page 60-64; 96pp: English.
PS	This is the nucleotide sequence of murine cDNA coding for
CC	sphingosine-1-phosphate lyase (SPL, see AAY05826). SPL cDNA was
CC	obtained from an EST from mouse early embryonic cells. SPL
CC	catalyzes the cleavage of sphingosine-1-phosphate into inactive
CC	metabolites. Sphingosine-1-phosphate is an endogenous tumour
CC	suppressor lipid that potentially inhibits breast cancer cell growth
CC	and invasiveness, while not affecting the growth of non-tumour
CC	cells. Mouse and human SPL polynucleotides (see AAX25666-67) and
CC	polypeptides (see AAY05826-27) are claimed. Methods are provided for
CC	preparing SPL using transformed or transfected host cells. Also
CC	provided are methods for utilizing SPL polypeptides for identifying
CC	agents that modulate SPL activity. An SPL inhibitor will inhibit
CC	growth of cancer cells, especially breast cancer cells. SPL
CC	inhibitors, including polynucleotides preventing expression of SPL
CC	genes, or antibodies against SPL, can also be used to prevent the
CC	development and/or metastasis of cancer, especially where the
CC	inhibitor is linked to an antitumour or antiestrogen receptor
CC	antibody. Detection of alterations in an endogenous SPL sequence
CC	can be used to diagnose cancer, and to assess the prognosis for
CC	recovery.
CC	xx xx
SQ	Sequence 1707 BP; 460 A; 376 C; 440 G; 431 T; 0 other:
Query Match	74.9%; Score 1278.2; DB 20; Length 1707;
Best Local Similarity	84.3%; Pred. NO. 0;
Matches 1439; Conservative	0; Mismatches 268; Indels 0; Gaps 0;
OY	1 ATGGCTACACAGACCTTGATGTTGAAGCCTTGAAGCCCTACTTAGAGATTGGAA 60
Dd	1 ATGCCCGGAMCCGACCTCTCAAGCTGAAGGACTTCGAGCCCTAATTGTGGAGTTTGGAA 60
OY	61 GTATACTCCAAAAGCCAGAATTATGTAATGAGACAATTGCACCACCAAGTATGAGCCCTG 120
Dd	61 TCTTATTCACAAAAAGCCAGAATAATGTGTAATGATGATTTGCACCAATAATGAGCCCTG 120
OY	121 CAGCTAATTCGATGGAGTGTGTGTGACCCCTGCTGAATAGTCTGGGATATGAGTTTGTG 180
Dd	121 CAGCTCATTTGGCTGAGTGTCTCTGTGTACTGTGCTGCAATAGTCTGGGTATGAGCTTATC 180
OY	181 TTCCAGCCAGAGAGTTTATGTCGAAGCTTTAAAAAGAAATGTTTTAACTCACCGAAG 240
Dd	181 TTCCAGCCAGAGAGTTTATGCTTCGGTTTAAAAAAAATTTAACTTATCAGGAG 240
OY	241 ATGCCCATTAATGGTCGTAATATTCACAGACAAGTTGAACACCAAGCAGATGATTTAGC 300
Dd	241 ATGCCATTTATTTGACGCTTAATATGCAACAACAGGTGAGCAAAGCCAAGAGATCTTGTG 300

QY	301	AAGAACATGTCATTTCTCCGAAAGTGGACAAAGAGTATGTGMAAGCTTTACCTCCCAAGGT	360
Db	301	AAGAACAATGCCATTTCTCTAAAGGTGACAAAGGATTATGTGAAACCTCTCCCTGTCAAGGT	360
QY	361	CTGACCTCATCTGCTGTTTGGAGAAACTTAAGAGATACAGCTCATATGAGACCTTCTGG	420
Db	361	ATGGGCACAGCTGAGAGTTCTGGAGAGACTCAAGAGATACAGTCCATGGATGTTCTCTGG	420
QY	421	CAAGAGGGGAGAGCCCTTGGAAACAGTGTACAGTGGGGGAGAGAACTCAGTACGCTCTT	480
Db	421	CAAGAGGGGAAAGCCCTCAGAGAGCTGTATACATGTGGGAAACGGAACCTCAGGAGCTGCTG	480
QY	481	GTGAAGGCTTATNGAGATTTTTCATAGAGATTAACCCCCGATCCAGATATATCTTCCACGA	540
Db	481	GTGACGGCTTATNGAGAAATTCACGtgGAGCAATTCACGTGCATCCGATATCTTCCCTGGA	540
QY	541	CTACACAGATATAGAGAGCAAGAAATTTGTAGAGATAGCTTTCTCCCTTCATAGGGAGACA	600
Db	541	TTGGCGAAGATTAGAGGCAAGAAATGCTTATAGATGACTTGTCTCCCTTCAATAGGGGACCA	600
QY	601	GATTCGTGTGATGTGTGACTTCTGGGGGAAACAGAAAGCATATCTGATGGCCTGCAAAACA	660
Db	601	GATTCCTGTGATGTGTGACTTCTGTGGGGAAACGGAAGCATCTGATGGCCTGCAAAAGCT	660
QY	661	TGTCCGGATCTTGCCCTTTGAGAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
Db	661	TACCCGGACTTGTGGCCTTGTAGAGAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
QY	721	GCCCCATGTGCAATTAACAAAGACCCAGTTACTTGGGATGAAATTTGTGGGGTCCCA	780
Db	721	GCCCCATGTGCAATTCGACAAAGACCCAGCTATTTTGGGATGAAATTTGTCCGACTTCCA	780
QY	781	TTGACGAAGATGATGAGAGTGGATGTGAGGGCAATGAGAAGAGCTATCTCCAGAAACT	840
Db	781	CTGAAAAAGAACATGAGAGTGGATGTGACAGGCAATGAAGAGAGCATCTCCAGAAACACA	840
QY	841	GCCATGCTCTGCTGTTCTTACCCACAGTTTCTCATGGTGTATATGATCTCTGCTCCCTAA	900
Db	841	GCTAAGCGGCTGTGTTACCCCAAGTTTCTCATGGTGTATGATGATCTCTGCTCCCAAA	900
QY	901	GTGGCGAAGCTGGCTGTCAAAATACAAATACCCTTCATGTGCGAGCTGTCTGGGAGGC	960
Db	901	GTGGCGAAGTTAAGCTGTACAGATATTAATATCCACCTCATGTGTGAGATGCTTGTGGGGGC	960
QY	961	TTTCTCATGCTCTTTATGAGAGAAAGCAGGATATCCCATCTGGAGCACCCATTTGATTTCCGG	1020
Db	961	TTTCTCATGCTCTTCATGAGAGAAAGCAGGATATCCCATCTGGAGAAACCATTTGATTTCCGG	1020
QY	1021	GTGAAGAGTGTACACAGATTTTACAGCTACACCCCTAAGTATGGTATATGCCCAAAAGGC	1080
Db	1021	GTGAAGAGTGTGACACAGATTTTACACCAATATCTCTAATAGTATGGTATATGGCTCTAAAGGT	1080
QY	1081	TCATCATTTGGTGTATATAGTACAAAGATACAGAGCTATACGATTTTCTGGTGCATACA	1140
Db	1081	TCATCATGTGTGTATATAGTACAAAGATACAGAGCTATACGAGCTATACGATTTTCTGGTGC	1140
QY	1141	GATTGGCAGGGTGGCATCTATGCTTCCCAACCATCGCAGGCTCACGGCCTGTGGGCATT	1200
Db	1141	GACTGCGAAGGTTGGTGTCTACAGCATCTCCAAAGCATAGCTGGCTACGGCCTGTGGGCATC	1200
QY	1201	AGCGAGCCTGTGGGGCTGCTGTATGACATCTTGGGTGAAACGGCTATGTTGAAGCTATCC	1260
Db	1201	ATTGTAGAGCTGTGGGCGGGCTTGTATGACATCTTGGGTGAAACGGCTATGTTGAAGCTATCC	1260
QY	1261	AAACGATATCAAAACATGTCGCGTCTCTCAAGTACAGAACTGGAAATATATCAAAAGGCATC	1320
Db	1261	AAACGATATCAAAACATGCTCGCTTCTTGAAATGAGACTGGAAACATCAAAACATC	1320
QY	1321	TTTGTGTTTGGGAATCCCAATATGTACATCTATGCTCTGGGATCCCGATTTTGTACATC	1380
Db	1321	TTTATTTTGGGATGATCCTCAATATGTCACTATATGTGCTGTGGATCCAAAGATTTTGTACATC	1380
QY	1381	TACCGACTATCAAACTGATACGTCTTAGGGGTGGAACCTTGAAACCACTGACGTTCCCA	1440

Query Match	71.3%	Score 1217	DB 20	Length 1467
Best Local Similarity	85.9%	Prod. No. 0		
Matches 1467	Conservative	0	Mismatches	0
			Indels	240
			Gaps	1
Sequence 1467 BP; 407 A; 328 C; 364 G; 368 T; 0 other:				
CC Inhibitor growth of cancer cells, especially breast cancer cells.				
CC They can also be used to prevent the development and/or metastasis				
CC of cancer, especially where the inhibitor is linked to an anti-tumour				
CC or anti-oestrogen receptor antibody.				
XX				
XX				
SO				
QY 1 ATGCCCTACACAGACCTCTGATGTGTGAAGCCCTTTGAGCCCTTATGAGATTTTGGAA				60
DB 1 ATGCCCTACACAGACCTCTGATGTGTGAAGCCCTTTGAGCCCTTATGAGATTTTGGAA				60
QY 61 GTATPACTCCACAAAAGCCCAAGAAATTTATGTAATGAGCATTTGACCAAGTATGAGCCCTG				120
DB 61 GTATPACTCCACAAAAGCCCAAGAAATTTATGTAATGAGCATTTGACCAAGTATGAGCCCTG				120
QY 121 CAGCTAATGTCATGAGAGTGTGTGTGTGACCCCTGCTGATAGTCTGGGGATATGATTTGTC				180
DB 121 CAGCTAATGTCATGAGAGTGTGTGTGTGACCCCTGCTGATAGTCTGGGGATATGATTTGTC				180
QY 181 TTCCAGCCAGAGAGATTATGTCATCAAGTTTAAAAAGAAATGTTTTAAGCTCACAGAGAG				240
DB 181 TTCCAGCCAGAGAGATTATGTCATCAAGTTTAAAAAGAAATGTTTTAAGCTCACAGAGAG				240
QY 241 ATGCCCATTTATTTGTCGTATGATTTCAAGACATTCGTAAGCAAGACCAAGATGATATTAGC				300
DB 241 ATGCCCATTTATTTGTCGTATGATTTCAAGACATTCGTAAGCAAGACCAAGATGATATTAGC				300
QY 301 AAGAATCATGTCATTTCTCTGAAGGTGACACAAGATGTGTAAGAGCTTTTACCTCCAGGGT				360
DB 301 AAGAATCATGTCATTTCTCTGAAGGTGACACAAGATGTGTAAGAGCTTTTACCTCCAGGGT				360
QY 361 CTGAGCCTATCTGCTGTTTGGAGAACTTAAAGGATGACACTCTATGAGAGCCTTCTGG				420
DB 361 CTGAGCCTATCTGCTGTTTGGAGAACTTAAAGGATGACACTCTATGAGAGCCTTCTGG				420
QY 421 CAAGAGGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAAAGCTCACTGAGCTCCTT				480
DB 421 CAAGAGGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAAAGCTCACTGAGCTCCTT				480
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATATCTTCCACAGA				540
DB 481 GTGAAGGCTTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATATCTTCCACAGA				540
QY 541 CTAGCAGATATGAGGCGAAGAAATTTGTAGGATAGCTTTTCCCTGTTAAATGGGGAGCA				600
DB 541 CTAGCAGATATGAGGCGAAGAAATTTGTAGGATAGCTTTTCCCTGTTAAATGGGGAGCA				600
QY 601 GATTGCTGTGATGTGACTCTTGTGGGGGAGACAGAAACATCACTATGAGCTGGCCGAAGCA				660
DB 601 GATTGCTGTGATGTGACTCTTGTGGGGGAGACAGAAACATCACTATGAGCTGGCCGAAGCA				660
QY 661 TGTGGGATCTGGCCCTTTGAGAAGGGGATCAAAAACCTCCAGAAATTTGGTGTCCCAAGT				720
DB 661 TGTGGGATCTGGCCCTTTGAGAAGGGGATCAAAAACCTCCAGAAATTTGGTGTCCCAAGT				720
QY 721 GCCCATGCTGCAATTTAAACAAAAGCAGCTTACTTTGGGATGAAAGATTGTGGGGTCCCA				780
DB 721 GCCCATGCTGCAATTTAAACAAAAGCAGCTTACTTTGGGATGAAAGATTGTGGGGTCCCA				780
QY 781 TTGACGAAGATGATGAGGTGATGTGAGGCAATGAAGAGCATATCTCCAGAGAACT				840
DB 781 TTGACGAAGATGATGAGGTGATGTGAGGCAATGAAGAGCATATCTCCAGAGAACT				840
QY 841 GCCATGCTGCTGCTTTTACCCACAGTTTCCCTATGCTAATAGATCTGTCCCTGAA				900
DB 841 GCCATGCTGCTGCTTTTACCCACAGTTTCCCTATGCTAATAGATCTGTCCCTGAA				900
QY 901 GTGGCAAGCTGTGCTGTAATACAAATACCCCTTCAATGTGCAGAGCTTGTCTGGAGGC				960
DB 901 GTGGCAAGCTGTGCTGTAATACAAATACCCCTTCAATGTGCAGAGCTTGTCTGGAGGC				960

Db 901 GTGGCCAGCTGGCTGTCAATATCAAAATACCCCTTCATGTGACACCTGTGTGGAGGC 960
 QY 961 TTCCATCGCTCTTATGAGAAAGCAGATACCACTGGAGCACCATTGATTCGG 1020 -
 Db 961 TTCCATCGCTCTTATGAGAAAGCAGATACCACTGGAGCACCATTGATTCGG 1020
 QY 1021 GTGAAGGCTGTAACGACATTTGAGTACACCCATTAATGATGCTGATTCG 1080
 Db 1021 GTGAAGGCTGTAACGACATTTGAGTACACCCATTAATGATGCTGATTCG 1080
 QY 1081 TCATCATGTGTGTATAGTACAGAAAGTACAGAAATCATGTTCTTCTGATACA 1140
 Db 1060 ----- 1059
 QY 1141 GATTGGCAGGTGGATCTATGCTTCCCAACCATCGACGGCTCAGGGCTGGGCAT 1200
 Db 1060 ----- 1059
 QY 1201 AGCGACGCTGTGGGCTGCTTGTATGACACTTGGTGAACGGCTATGTTGAAGCTACC 1260
 Db 1060 ----- 1059
 QY 1261 AAACAGATCATCAAAACTGCTGCTTCTCAAGTACAGAACTGGAATATCAAGGCATC 1320
 Db 1060 ----- 1080
 QY 1321 TTTGTTTTGGGAATCCCAATTTGATCATCTGCTGTGGATCCCGTATTTTGAATC 1380
 Db 1081 TTTGTTTTGGGAATCCCAATTTGATCATCTGCTGTGGATCCCGTATTTTGAATC 1380
 QY 1381 TACCGATATCAAACTGATGACTGTAAGGGGTGACACTTGAACAGTTGCACTTCCCA 1440
 Db 1141 TACCGATATCAAACTGATGACTGTAAGGGGTGACACTTGAACAGTTGCACTTCCCA 1440
 QY 1441 CCCAGATTCATTTTGCATACATTAACAGCCGGAAGAGTATGATATACATTC 1500
 Db 1201 CCCAGATTCATTTTGCATACATTAACAGCCGGAAGAGTATGATATACATTC 1260
 QY 1501 CTAAAGGACATTCGAGATCTGTCACTCAATCATGAAGATCTTAAAGCGAAGCACA 1560
 Db 1261 CTAAAGGACATTCGAGATCTGTCACTCAATCATGAAGATCTTAAAGCGAAGCACA 1320
 QY 1561 GGAATGGTGCATCATGCAATGAGCCGAGACAACTGTGACAGAAATATGTTGAGAA 1620
 Db 1321 GGAATGGTGCATCATGCAATGAGCCGAGACAACTGTGACAGAAATATGTTGAGAA 1380
 QY 1621 TTGTCTCAGTCTTCTTGGACAGCTTGTACAGACGACGACATGTACCCAGGAGCCAG 1680
 Db 1381 TTGTCTCAGTCTTCTTGGACAGCTTGTACAGACGACGACATGTACCCAGGAGCCAG 1440
 QY 1681 ATGAATGTTTTCGAAACCCCACTGA 1707
 Db 1441 ATGAATGTTTTCGAAACCCCACTGA 1467
 RESULT 8
 ID ABL14565 standard; cDNA; 1746 BP.
 AC ABL14565;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide seq ID NO 38177.
 XX
 KW Drosophila: developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PR (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PMD, Myers EW;
 PI WPI: 2001-655860/75.
 DR P-PADB; ABB70462.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1; SEQ ID NO 38177; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB101840-AB116175).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 1746 BP; 393 A; 471 C; 484 G; 398 T; 0 other;
 Query Match 23.5%; Score 401.6; DB 23; Length 1746;
 Best Local Similarity 55.4%; Pred No. 2.8e-117;
 Matches 864; Conservative 0; Mismatches 684; Indels 12; Gaps 4;
 QY 110 ATGAGCCCTGGGACGTAATGATGAGTGTGTGACCCCTGATAGTCTGGGAT 169
 Db 179 AGAGCCCTGGGAGTGGGACCATCATCGGCCACACCGGCTGCTGGAGCGCTGCTCT 238
 QY 170 ATGATGTTGCTTCCAGCCAGAGATGTTATGCTCAAGGTTTAAAGAAATGTTTAAAC 229
 Db 239 GGAGTGTGATCTGCGAGATGAATACTTAACTTGAATCTGTCGCAAGCCCTCTTAAAT 298
 QY 230 TCACAGGAAGATGCCATTAATGTCGTAAGATTAACAAGTTGAACAGACCAAG 289
 Db 299 TTGCCAAGAAGATTCAGCGCGTGTGTCGTCAGGTGAGACTGAATTTGCCAAGCCAAA 358
 QY 290 ATGATATTAGCAAGAATCATGTCATTCCTGAAGTGAACAGATATGTAAGCTTTAC 349
 Db 359 ACGACTTCGAGACGAAATCAAAAAGCAAGCCACCTTACTCTACCTGGAACCTCTGC 418
 QY 350 CCTCCAGGCTGAGACCTATCTGCTGTTTGGAGAAACTTAAAGAGTAC---AGTCTTA 406
 Db 419 CCGAGAAGGAGCTCAACAAGAGAGAGATCTCCGATGTTGATGAGACCTGAAGACG 478
 QY 407 TGGACGCTTCTGGCAAGAGAGAGAGAGCTCTGGAACAGTGTACAGTGGGAGAGAAAC 466
 Db 479 GTACATCAAACTGGCGCTGATGTCGTGATCTGCGCGGCTTACAGGCTCAAGCCGTGAT 538
 QY 467 TCACGTGAGCTCTTGTGAAGCTTATGAGATTTTGCATGAGATTAACCCCTGCATCCAG 526
 Db 539 TGGTGGAGCTCTCACTGAAGTGTACGGAAGGCGCTCTTACCAATCCCTTGCAGCGAG 598
 QY 527 ATATCTTCCAGAGCTACCAAGATAGAGCGAAGAAATTTGTAGATAGTCTTCCCTGT 586
 Db 599 ATCTTTTCCCGGAGTTTGAAGAAATGAGCGGAGAGTGTGCGCATGATCAACCTGT 658
 QY 587 TCAATGGGAGCAGATTCGTGTGGATGTGTGATCTTCTGGGGAACAGAAACATATACCA 646
 Db 659 TCATATGGAATCACTGACGAGCTGTGGAACCATGACACCGGCGCACCAATCATTTGTAA 718

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QY 647 TGGCTGCAAGCATGCGGGATCTGGCCCTTTGAG---AAGGGGATCAAACTCCAGAAA 703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 719 TGGCATTGAAGCGGATACAGGGATTTGCTGAGAGTACAGGAGATCACAGGCCAACA 778
QY 704 TTTGGCTCCCAAGATGCCATGCTGATTTTAAACAAGACCAAGTACTTTGGGATGA 763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 779 TCTGTGGCTTAAGACGCTCCAGCGCCCTTCGCAAGGGCGGTCACTACTTTAAATATCC 838
QY 764 A---GATTTGGCGGGTCCATTTGACAGATGATGAGATGATGAGGGCAATGAGAA 820
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 839 ACCTGGCATCCGTGGATGATGATGATCCGAGACCTACGAGATGATTAAGAAATTTCAAC 898
QY 821 GACCTATCTCCAGAAACACTGCTGCTGTTCTTACCCACAGATTTCTCATGATG 880
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 899 GTGCAATTAAACAGAAACAGATTTCTGTGTTGGGTGCTGTCGAACTTCCCATATGAA 958
QY 881 TAATAGATCTGTCCTGAAGTGCCAGCTGGCTGCAATATCAAAATACCCCTTATG 940
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 959 CCAATCGATGACATGAAAGTATGCGCCCTTTGGCGCTTAAGTACGACATTCGCGTCACG 1018
QY 941 TCGACGCTTGTGCGGAGCTTCTCCTCATGCTTTTATGAGAAAGCAGATACCCATGG 1000
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1019 TGAACGCTCTGCTGGGAGCTTTGTGGCTTGTGCGCACGCGGCTATTAAGCT-- 1076
QY 1001 AGCACCATTGATTTCCGGGTGAAGGTAAACACAGCATTTGAGTACACCATTAAGT 1060
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1077 -GGTCCCTTCGACTTTGAGTCAAGGAGTACGACATATCTCCGCTGATACCACTAAGT 1135
QY 1061 ATGCGTATGCCCCCAAAAGCTCATGTTGTTGTATGATGACAGAGATGACAGAACT 1120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1136 ATGCTTTCGCGCCCAAGGATGATCGGTATCTTCTGCGACAAAGATACAGAGACC 1195
QY 1121 ATGAGTCTCTGCGATGACAGATTTGGAGGAGTGCATCTATGCTCCCAACCATTCAG 1180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1196 ATGACCTGCTGCTGAGTACTGAGTGGGCTGCGCGCTGTGTTGGTCTCCACACTCAAG 1255
QY 1181 GCTACAGGCTGTTGATGATGAGCAGCAGCTGTTGGGCTGCTGATGATGATGATGATG 1240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1256 GTTCCGCTGCGGAGATATATGCGCGCTGCTGAGTACATGATGATGATGATGATG 1315
QY 1241 AGCGCTATGTTGAAGTACCAAAACAGATCAAAACTGCTCGCTTCTCAAGTACAGAAC 1300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1316 ATGCTTATCGAAGCAGCACTAAGGCACTGTTGATGATGAGCGGCTATATGAGAGGGCG 1375
QY 1301 TGGAAATATCAAGGATCTTTGTTGGGAATCCCAATTCCTCACTGATGCTCTGG 1360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1376 TTGCGCAGATGATGATGATCTTTATCTTTGGCAAGCCAGCTACTTCAATGATGCTCTGG 1435
QY 1361 GATCCGCTGATTTTGAATCTTACGATCACTAACAAGTGAAGTGAAGTGAAGTGAAGT 1420
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Db 1436 GTTCCATATGTTTGAATCTTTCCGGCTATCGGATGATGATGATGATGATGATGATG 1495
QY 1421 TGAACAGTTCAGTTCACCAAGTATTTATTTTGTGATGATGATGATGATGATGATG 1480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1496 TGAATGCGTGCAGTTCATCTGATTCACACCTGCTGATGATGATGATGATGATGATG 1555
QY 1481 AAGAGATATATCAAGGATCTTCAAGGATGATGATGATGATGATGATGATGATGATG 1540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1556 CCGGAGTCCGCGATTAATTTATTTGCGATGATGCGACCTGATGCGGCGGATGATGAGG 1615
QY 1541 ATCTTAAGGAGAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1600
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Db 1616 ATCCGCGGAGCGCGCTGTTGAAAGATGATGATGATGATGATGATGATGATGATGATG 1675
QY 1601 ACAGGATATGTTGCGAATTTGCTCTGATGATGATGATGATGATGATGATGATGATG 1660
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Db 1676 ACCGTTGCGATGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1735
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RESULT 9
ABLI4555
ID ABLI4555 standard; cdna: 1782 bp.
XX
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AC ABLI4555;
XX
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38147.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
XX P-PsDB: ABB70452.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 38147; 21bp + Sequence Listing: English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABLI16175-ABLI30511), expressed DNA
XX sequences (ABLI01840-ABLI16175) and the encoded proteins
XX (ABBI7737-ABBI2072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1782 bp; 410 A; 493 C; 486 G; 393 T; 0 other:
XX
XX Query Match 23.5%; Score 401.6; DB 23; Length 1782;
XX Best Local Similarity 55.4%; Pred. No. 2.8e-117;
XX Matches 864; Conservative 0; Mismatches 684; Indels 12; Gaps 4;
XX
XX 110 ATGAGCCCTGGCAGCTAATTCATGAGTGTCTGTGGACCTCTCTATGCTGGGGAT 169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 215 AGGAGCCCTGGCAGTGGCCACATCAAGCCACACGCTGTGGAGGCTGTGGCTCT 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 170 ATGAGTTGTTCTTCCAGCAGAGAGTTTATGCTCAAGGTTTAAAGAAATGTTTAAAGC 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 215 AGGAGCCCTGGCAGTGGCCACATCAAGCCACACGCTGTGGAGGCTGTGGCTCT 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 275 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 275 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 230 TCACAGGAAGATGCCCATTAATGTTGCTAAGATTTCAAGACAACTTGAAGCAAGC 289
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Db 335 TTGCGCAAGAGATTCAGCGCGTGTGCTGATGATGATGATGATGATGATGATGATGATG 394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 290 ATGATATTAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 395 ACAGCTTCGAGACGAAATCAAAAGAGACAGCCACTTACCTACTCGAAACCTCTGC 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 350 CTTCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 455 CCGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 407 TGAAGCCCTTCTGGCAAGAGGAGAGCCCTGTGGAACAGTGTACAGTGGGAGAGAGAGC 466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 515 GTCACTACAACTGGCGTATGCTGTATCTGCGCGGTCTACGCTACAAAGCCTGATC 574
Oy 467 TCACAGACTCTCTTGTGAAGCCTATGAGATTTTGCATGAGAGTAAACCCCTGCATCCG 526
Db 575 TGGTGAAGCTGCTCACTGAGTACGGCAGAGCCTCTCTACACCAATCCCTTGCCAGCAG 634
Oy 527 ATATCTCCCAAGACTACGACAGATAGAGAGCAAAATTTGAGATAGCTTTGCTCCGT 586
Db 635 ATCTTTCCCGGAGTTTGCAAAATGAGAGCGAGAGTGTGCGCATGCGATCACAACCTGT 694
Oy 587 TCAATGGGGAGCCAAATTCGTGTGATGTGTACTCTTGGGGGAGACAGAAAGCATATCTCA 646
Db 695 TCCATAGGAAAGTCAACCCAGCTGTGAGACCATGACCGCGGACCGCAATCCATTGTAA 754
Oy 647 TGGCTGCAAGCATGTGCGGATCTGGCCTTTGAG--AAGGGATCAAAACTCCAGAA 703
Db 755 TGGCCATGAGGCGTACAGAGATTTTCGTAGAGATACAGAGGATACACAGGCCAAGAA 814
Oy 704 TTGTGGCTCCCAAGAGTGGCTGCAATTTAACAAAGCAGCCAGTTACTTTGGGATGA 763
Db 815 TCGTGGTCCCTAAGACGGGTCCACGGGCTTCGACAAAGGCGGTGAGTACTTTAATATCC 874
Oy 764 A---GATTTGGGGTCCCATTTGAGAAAGATGATGAGTGTGATGTGAGGCGCAATGAGA 820
Db 875 AGCTGCGATCGGTGATGTAGATCCGAGACCTACGAAATGGACATTAAGAAATTCAAAC 934
Oy 821 GAGCTATCTCCAGAAACACTGCGATCTGTCTTCTACCCACAGTTTCCCTCATGTG 880
Db 935 GTTCCATTAAACAGAAACAGATTTCTGTGGTGGTGTCTCTCGAACTTCCCTATGGA 994
Oy 881 TAATGATCTCTCCCTGAGTGGCCAAAGCTGGCTGTCAATACAAATACCCCTTCATG 940
Db 995 CCATGATGATGATCAAGATATCGCGCTTTGGGGGTAAAGTACGATTCCTCCGTGCAAG 1054
Oy 941 TCGACGCTTGTGGGAGGCTCTCATGCTTTATGAGAGAGAGATCCCAACCTG 1000
Db 1055 TGGAGCCCTGCTGGGAGCCTTTGTGTGCTTGTGCTCGCAACGCCGCTTAAGCT-- 1112
Oy 1001 AGCACCATTGATTTCCGGGTGAAGAGTGTAAACAGATTCCTGACGTGACCCATTAAGT 1060
Db 1113 -GCTTCCCTTTCGATTTGAGTCAAGGAGTACCAAGTATCTCCGTGATACCAAGT 1171
Oy 1061 ATGCTATGCCCCAAAGGCTCATCTGTTGTGTATGATGATGATGATGATGATGATGAT 1120
Db 1172 ATGCTTTCGCGCCCAAGGATCATGCTGATCTTACTCGGACAAAGATGACAAAGATC 1231
Oy 1121 ATCACTTCTTCTGATACAGATGATGAGGAGGATCATATGATTCGCCCAACATCGGAG 1180
Db 1232 ATCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291
Oy 1181 GCTCAAGGCTGTGGCATTTAGCGAGCCTGTTGGGCTGCTTGTATGATGATGATGATGAT 1240
Db 1292 GTTCCGCTCGGAGGATATATCGCGCTGCTGGGCTACATGATGATGATGATGATGATGAT 1351
Oy 1241 AGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1300
Db 1352 ATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1411
Oy 1301 TGGAAATATCAAGGATCTTTGTTTGGGAATCCCAATGTCATGATGATGATGATGATGAT 1360
Db 1412 TTGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1471
Oy 1361 GATCCGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1420
Db 1472 GTTCCAAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1531
Oy 1421 TGAACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1480
Db 1532 TGAATGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1591
Oy 1481 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1540
Db 1592 CCGGAGTCCGATTAATTCATTCGCGATGTGCGGACGCTGTACGGGCGGATGATGATGATGAT 1651

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Oy 1541 ATCTTAAGCGAAGACACAGGAATGGTCCATCTATGCGCCAGACACTGTTG 1600
Db 1652 ATCCGCGGACAGCCGCTGCTGGAAGATGGCTCTTACGGCATGCGACAGACATACCGG 1711
Oy 1601 ACAGAAATATGTTGCTCAGATTTGCTCTGTTTGGACAGCTTTGACACACCGACA 1660
Db 1712 ACCGTTGCGTGTATCGAGAGTACTCGCCATATCTCTGCTACATGATGATGATGATGAT 1771

RESULT 10
AAD06842
ID AAD06842 standard; DNA; 2060 BP.
XX
AC AAD06842;
XX
XX 03-AUG-2001 (first entry)
XX
XX Drosophila melanogaster sphingosine phosphate lyase (SPL) cDNA.
DE
XX Fruit fly: sphingosine phosphate lyase; SPL; metazoan; insect;
KM worm; pesticidal agent; therapeutic; pesticide; drug target; ss.
XX
XX Drosophila melanogaster.
XX
XX Key Location/Qualifiers
XX CDS 110..1747
XX FT /tag= a
XX FT /product= "sphingosine phosphate lyase (SPL)."

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Db      785 TTGCTCCCGTACGACATGCTGGTTTGACAAAGCTGCTATTACTTTGGCATGAGC 844
Qy      767 TTGTGGGGTTC---CCATTGACGAAGATGATGAGGAGGATGAGGGCATGAGAG 823
Db      845 TAGCCACGCTGAGTATGATCAACGACATATCAAGTGGACCTGGGAAAATAAAT 904
Qy      824 CTATCTCCAGACACTGCTGCTGTTCTTACCCAGATTTCCATGTTGTA 883
Db      905 TCATCAATAGAACACATTTTACTGTGCTCCGCTCCCAACTTTCATGATTTG 964
Qy      884 TAGATCTCTGCTGAGTGGCCAGCTGCTCAATATCAAAATACCCCTTCATGTCG 943
Db      965 CCGATGATTTGAAGATTTGGTAAATAGCACAAAATAATTAACCTTTCATGACGTCG 1024
Qy      944 ACCGTGCTCGGAGGCTTCTCATGCTCTTTATGGAAGAACAGATACCCTGAGC 1003
Db      1025 ACAGTGTCTAGGCTTCTTTATGTTTCAATTTATGAAAAGGCTGTGTAATAAATCTGC 1084
Qy      1004 ACCCATTTGATTTCCGGGTGAAGGTATACACAGCATTTTACGCTGACCCCATATGATG 1063
Db      1085 CATTACTTGACTTATAGTCCCGGAGTCACTCAATATCATGTGACACTCAATATATG 1144
Qy      1064 GCTATGCCCCAAAGGCTCATATGCTGTTGATATGACAAAGATACAGAACTATC 1123
Db      1145 GATTTGACCAAAAGGCTCGTCAATATGATATAGAAAAGGAGCTTACGAATGCATC 1204
Qy      1124 AGTTCTTCGTGATACAGATTTGGCAGGTTGGCATCTATGCTTCCCAACCATGCGAGCT 1183
Db      1205 AGATTAAGTAAATCTGCTTGGAGTGGCTGGGCTTATATGAGCTCTCCATTAATGACAGGCT 1264
Qy      1184 CACGCGCTGCTGATTAAGCCAGCCGTTGGGCTGCTGATGACACTTGGTGAAGC 1243
Db      1265 CAGAGCTGGTGTATGTTGATGTTGGGCTATGAGTCAATATGATGATGATGATG 1324
Qy      1244 GCTATGTTGAAGTACCAAAAGATCATCAAACTGC---TCGCTTCTCAAGTCAGAAC 1300
Db      1325 GGTACATATGAGTGTGCGCAAGAAATAGTCCGTGCGCAAGAAATGTTAAATAATCATCTC 1384
Qy      1301 TGGAAATATCAAAAGCATTTGTTTGGGAATCCCAATGTCCTGCTATGCTCTG 1360
Db      1385 AGGAAACATTTCCAGACCTGAATATATGAGCAACCTTAGATTTCACTTTCATTTT 1444
Qy      1361 GATCCGCTGATTTGACATCTACGACATCAAACTGATGACTGTAGGGGTGGAAT 1420
Db      1445 CTTCAAAGACCTTGAACATACAGAACTATCTGACAGTGTGTCCAAAGAGGCTGGCAT 1504
Qy      1421 TGAACCAAGTTCAGTCCACCCAGTATTTCAATTTCTGATCATACTTCTACAGCCC 1477
Db      1505 TCAATGCCCTACAAAGCCGTTGCACTACACATGGCTTCACGAGATTGAGCGCTC 1561

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RESULT 13
AAH29742
ID AAH29742 standard; DNA; 2270 BP.

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XX      AAH29742:
XX      27-JUL-2001 (first entry)
XX      S cerevisiae apoptosis associated coding sequence YDR294C.
XX      DE      yeast; fungus; apoptosis; infection; proliferative disease;
XX      KM      vaccine; autoimmune disease; ischemia; neurodegeneration; ds.
XX      OS      Saccharomyces cerevisiae.
XX      PN      WO200102550-A2.
XX      PD      11-JAN-2001.
XX      PF      03-JUL-2000; 2000WO-BE00077.
XX      PR      01-JUL-1999; 99EP-0870141.

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XX      (JANC) JANSSEN PHARM NV.
XX      Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL.
XX      Nelissen BJM, Reekmans RJ.
XX      WPI: 2001-367042/38.
XX      P-PSDB: AAG70706.
XX      DR      Yeast and fungal nucleic acids encoding proteins involved in a pathway
XX      PT      leading to programmed cell death, useful for treating proliferative
XX      PT      disorders, yeast and fungal infections, or for preventing apoptosis in
XX      PT      certain diseases -
XX      PS      Claim 1; Fig 1: 218pp; English.
XX      CC      The present invention provides the protein and coding sequences of a
XX      CC      number of apoptosis associated proteins from the yeast Saccharomyces
XX      CC      cerevisiae and the fungus Candida albicans. These can be used to identify
XX      CC      treatments for fungal and yeast infections, for proliferative diseases
XX      CC      and for apoptosis related diseases such as autoimmune diseases, ischemia
XX      CC      and neurodegeneration. The present sequence is one of the S. cerevisiae
XX      CC      coding sequences of the invention.
XX      SQ      Sequence 2270 BP; 707 A; 450 C; 467 G; 646 T; 0 other;
XX
Query Match      15.0%; Score 256.2; DB 22; Length 2270;
Best Local Similarity 55.0%; Pred. No. 1.2e-70;
Matches 592; Conservative 0; Mismatches 473; Indels 12; Gaps 4;
Qy      413 CTTTCTGCAAGAGGAGAGACCTCTGACACAGTATGACAGTGGAGAGAGAGCTCAGT 472
Db      985 CCAATGGAAGAAAGAAAGGTCTGCTGCGCTTACCAAGGTGATGATGATGATGATC 1044
Qy      473 AGCTCTTGTGAAGCTTATGAGATTTGATGAGATTAACCCCTGATCAGATATCT 532
Db      1045 ACTTACAAACAAATGCAATGACAAATAATGCGTTGCCAATTAATCAATTCCTCATCT 1104
Qy      533 TCCAGAGATACGCAATATGAGGCAAGAAATGAGAGATAGCTTGTCCCTGTTCAAT 592
Db      1105 TTCTGCGGTACGTAATATGATATCCAGATGTTTCTATGTTTAAAGATGTTTAAATG 1164
Qy      593 GGGGACAGATTTCTGTGATGTGTG---ACTTCTGGGGGAAACAGAAAGCATCTCATGG 649
Db      1165 CCCCTTGATATACAGTGTGTTGTTACCAACTTCAGGTGATGAGATTCCTGTTTATG 1224
Qy      650 CTTCGAAGCATGTGCGGATCTGCGCTTTGAGAA---GGGATCAAAATCTCAGAAATTG 706
Db      1225 CATGCTGAGCGCTTAAATATGATGCTCTCATCATCTGTGAAATCCAGAACCAATAAT 1284
Qy      707 TGGCTCCCAAGAGGCCATGCTGATTTAAACAAAGCAGCCAGTTACTTTGGATGAGA 766
Db      1285 TTGCTCCGTTACTGCAATGCTGCTGGTTTGCACAAAGCTGCTTATTTAGCTTGGCATGAGC 1344
Qy      767 TTGTGCGGGTTC---CCATTGACGAAGATGATGAGTGTGAGGGCAATGAGAGAG 823
Db      1345 TAGCCACGCTGAGACTGATGCCAAGCATATCAAGTGAAGAGCTGGAAAGTGAATAAT 1404
Qy      824 CTATCTCCAGACACTGCTGCTGCTGTTTACCCACAGATTTCTCATGTTGTA 883
Db      1405 TCATCAATAGAACACATTTTACTGTGCTGCTGCTCCCAAACTTCTCATGTTGTA 1464
Qy      884 TAGATCTGTCCTGGAAGTGGCCAGCTGCTCAATATCAAAATATCCCTTCATGTCG 943
Db      1465 CCGATGATTTGAAGGATTTGGTAAATAGCACAAAATAATATTAACCTTCTTTACAGCTGC 1524
Qy      944 ACAGTGTCTGGAAGCTTCTCATGCTTTTATGAGAAAGCAGATACCCACTGAGC 1003
Db      1525 ACAGTGTCTAGGTTCTTTATGTTTATGTTTATGAGAAAGGCTGTGTAATAAATCTGC 1584
Qy      1004 ACCCATTTGATTTCCGGGTGAAGGTTAAACGACATTTTCACTGACACCATATGATG 1063
Db      1585 CATTACTTGACTTATGAGTCCCGGAGTCACTCAATATCATATGATGACACTCATTAATATG 1644

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Db 3323 GTCAAGGTTCCCGCGAGGTAATATCGCGCTGCGGTACCATGATGAGCTTT 3382
QY 1234 GGTGAGAAAGGCTATGTTGAAGCTACCAACAGATCATCAAAACTGCTGCTTCCCAAG 1293
Db 3383 GGCTATGATGTTATCTGGAAGCCACTAAGCCCATTTGTGATACGGCGGCTATATCGAG 3442
QY 1294 TCAGAACTGGAATAATATCAAG 1315
Db 3443 AGGGGGTAAGTTGTATCAAG 3464

Search completed: October 6, 2003, 13:39:21
Job time : 487 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:50:19 ; Search time 40 Seconds

(Without alignments)
2246.624 Million cell updates/sec

Title: US-10-053-510-8

Perfect score: 2977
Sequence: 1 MFSTDLMLKAFEPYLEILE.....LYSDNYTGSQNGSPKPH 568

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2977	100.0	568	12 US-10-197-073-4	Sequence 4, App11
2	2977	100.0	568	12 US-10-053-510-8	Sequence 8, App11
3	2977	100.0	568	12 US-10-286-175-4	Sequence 4, App11
4	2959	99.4	568	10 US-09-740-369-2	Sequence 2, App11
5	2959	99.4	568	12 US-10-053-510-18	Sequence 18, App11
6	2553	85.8	568	12 US-10-197-073-2	Sequence 2, App11
7	2553	85.8	568	12 US-10-053-510-6	Sequence 6, App11
8	2553	85.8	568	12 US-10-286-175-2	Sequence 2, App11
9	2498	83.9	488	12 US-10-197-073-10	Sequence 10, App11
10	2498	83.9	488	12 US-10-053-510-10	Sequence 10, App11
11	2498	83.9	488	15 US-10-286-175-10	Sequence 10, App11
12	1344	45.1	545	12 US-10-053-510-16	Sequence 16, App11
13	1082	36.3	552	12 US-10-053-510-11	Sequence 11, App11
14	1008	33.9	542	12 US-10-197-073-6	Sequence 6, App11
15	1008	33.9	542	12 US-10-053-510-4	Sequence 4, App11

16	1008	33.9	542	15 US-10-286-175-6	Sequence 6, App11
17	1007.5	33.8	589	12 US-10-197-073-8	Sequence 8, App11
18	1007.5	33.8	589	12 US-10-053-510-2	Sequence 2, App11
19	1007.5	33.8	589	15 US-10-286-175-8	Sequence 8, App11
20	355	11.9	76	10 US-09-740-369-4	Sequence 4, App11
21	244.5	8.2	509	12 US-10-167-547C-4	Sequence 4, App11
22	244.5	8.2	529	12 US-10-167-547C-6	Sequence 6, App11
23	233.5	7.8	496	12 US-10-006-852-12	Sequence 12, App11
24	233	7.8	500	15 US-10-006-852-16	Sequence 16, App11
25	228.5	7.7	496	15 US-10-006-852-14	Sequence 14, App11
26	227.5	7.6	496	15 US-10-005-602-2	Sequence 2, App11
27	227	7.6	454	15 US-10-156-761-1138	Sequence 1138, A
28	227	7.6	502	15 US-10-006-852-2	Sequence 2, App11
29	226	7.6	494	15 US-10-006-852-4	Sequence 4, App11
30	219.5	7.4	498	12 US-10-167-547C-2	Sequence 2, App11
31	216.5	7.3	470	15 US-10-156-761-12189	Sequence 12189, A
32	211.5	7.1	494	15 US-10-006-852-10	Sequence 10, App11
33	209	7.0	502	15 US-10-006-852-18	Sequence 18, App11
34	202	6.8	500	15 US-10-006-852-6	Sequence 6, App11
35	198	6.7	493	15 US-10-006-852-8	Sequence 8, App11
36	174.5	5.9	505	15 US-10-156-761-12806	Sequence 12806, A
37	167	5.6	480	15 US-10-156-761-13740	Sequence 13740, A
38	155.5	5.2	488	12 US-10-032-585-7216	Sequence 7216, App
39	150.5	5.1	393	10 US-09-712-363-264	Sequence 264, App
40	145	4.9	241	10 US-09-978-248-11	Sequence 11, App11
41	144.5	4.9	389	15 US-10-156-761-10293	Sequence 10293, A
42	144	4.8	393	9 US-09-846-590B-14	Sequence 14, App11
43	139	4.7	453	12 US-10-342-224-118	Sequence 118, App
44	131	4.4	457	15 US-10-156-761-13584	Sequence 13584, A
45	131	4.4	585	15 US-10-038-686-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-10-197-073-4
Sequence 4, Application US/10197073
Publication No. US20030166897A1
GENERAL INFORMATION:
APPLICANT: Sabo, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197, 073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dravner, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116, 402D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid

TOPLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-10-197-073-4

Query Match 100.0%; Score 2977; DB 12; Length 568;
Best Local Similarity 100.0%; Pred. No. 2.9e-287;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIIVGSEYV 60
DB 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIIVGSEYV 60
QY 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKRDISKMSFLKDKYKVALPSOG 120
DB 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKRDISKMSFLKDKYKVALPSOG 120
QY 121 LSSAVLEKLEKSSMDAFWQGRASGYVSGEEKLTLLVKAAGDFAMSNPLHDPDIFG 180
DB 121 LSSAVLEKLEKSSMDAFWQGRASGYVSGEEKLTLLVKAAGDFAMSNPLHDPDIFG 180
QY 181 LKRIEAEIVRIACSLFNGPDSGCVTSGETSILMACACRDIAFEKGIKTPETIAPQS 240
DB 181 LKRIEAEIVRIACSLFNGPDSGCVTSGETSILMACACRDIAFEKGIKTPETIAPQS 240
QY 241 AHAATFNKAASYFGMKIVRVPLTKMMEVDVRAARRAISRTAMLCVSTQFPFGVIDPYVE 300
DB 241 AHAATFNKAASYFGMKIVRVPLTKMMEVDVRAARRAISRTAMLCVSTQFPFGVIDPYVE 300
QY 301 VAKLAVKTKIPLHVDACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKTKIPLHVDACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSLVLYSDKKYRNYOFEVDTDQGGIYASPTIAGSRPGISAAACMAALMHFEGENGYEAT 420
DB 361 SSLVLYSDKKYRNYOFEVDTDQGGIYASPTIAGSRPGISAAACMAALMHFEGENGYEAT 420
QY 421 KOITATARFLKSELENIKIGIFVFGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
DB 421 KOITATARFLKSELENIKIGIFVFGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIKNKPKAKTTGATGATYAMAQTVDNRMAE 540
DB 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIKNKPKAKTTGATGATYAMAQTVDNRMAE 540
QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 2
US-10-053-510-8
; Sequence 8, Application US/10053510
; Publication No. US20030175939A1
GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrist, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-510-8

Query Match 100.0%; Score 2977; DB 12; Length 568;
Best Local Similarity 100.0%; Pred. No. 2.9e-287;

Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIIVGSEYV 60
DB 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIIVGSEYV 60
QY 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKRDISKMSFLKDKYKVALPSOG 120
DB 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKRDISKMSFLKDKYKVALPSOG 120
QY 121 LSSAVLEKLEKSSMDAFWQGRASGYVSGEEKLTLLVKAAGDFAMSNPLHDPDIFG 180
DB 121 LSSAVLEKLEKSSMDAFWQGRASGYVSGEEKLTLLVKAAGDFAMSNPLHDPDIFG 180
QY 181 LKRIEAEIVRIACSLFNGPDSGCVTSGETSILMACACRDIAFEKGIKTPETIAPQS 240
DB 181 LKRIEAEIVRIACSLFNGPDSGCVTSGETSILMACACRDIAFEKGIKTPETIAPQS 240
QY 241 AHAATFNKAASYFGMKIVRVPLTKMMEVDVRAARRAISRTAMLCVSTQFPFGVIDPYVE 300
DB 241 AHAATFNKAASYFGMKIVRVPLTKMMEVDVRAARRAISRTAMLCVSTQFPFGVIDPYVE 300
QY 301 VAKLAVKTKIPLHVDACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKTKIPLHVDACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSLVLYSDKKYRNYOFEVDTDQGGIYASPTIAGSRPGISAAACMAALMHFEGENGYEAT 420
DB 361 SSLVLYSDKKYRNYOFEVDTDQGGIYASPTIAGSRPGISAAACMAALMHFEGENGYEAT 420
QY 421 KOITATARFLKSELENIKIGIFVFGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
DB 421 KOITATARFLKSELENIKIGIFVFGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIKNKPKAKTTGATGATYAMAQTVDNRMAE 540
DB 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIKNKPKAKTTGATGATYAMAQTVDNRMAE 540
QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 3
US-10-286-175-4
; Sequence 4, Application US/10286175
; Publication No. US20030059922A1
GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/286,175
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Steven J.
REGISTRATION NUMBER: 43,058

```

; REFERENCE/DOCKET NUMBER: 200116.402C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-286-175-4

Query Match          100.0%; Score 2977; DB 15; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,9e+287;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTDLLMLKAFEPYLEILEVYSTKAKNYVNGHCTKYPEPMOLIAWSVYVTLTIWGYEFV 60
DB 1 MPSTDLLMLKAFEPYLEILEVYSTKAKNYVNGHCTKYPEPMOLIAWSVYVTLTIWGYEFV 60
QY 61 FQPELSMRFRKKCKEKLTRKMPITIGRKIODKLNTKDDISKMSFLKVDKEYVAKLPSSQG 120
DB 61 FQPELSMRFRKKCKEKLTRKMPITIGRKIODKLNTKDDISKMSFLKVDKEYVAKLPSSQG 120
QY 121 LSSSAVLEKLEKSSMDAFMOEGRASGTIVYSGEEKLTBLVKA YGDFAMSNPLHDPDPG 180
DB 121 LSSSAVLEKLEKSSMDAFMOEGRASGTIVYSGEEKLTBLVKA YGDFAMSNPLHDPDPG 180
QY 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
DB 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
QY 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
DB 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
QY 241 AHAANKAASYFGMKIVVPLTKMMEVDVRAAMRAISRNTAMLCSTQFPHGVDPVPE 300
DB 241 AHAANKAASYFGMKIVVPLTKMMEVDVRAAMRAISRNTAMLCSTQFPHGVDPVPE 300
QY 301 VAKLAVKKYKIPLHVDAICGGLIVMEKAGYPLEHPDFRYKGVTSISADTHKKYAPBK 360
DB 301 VAKLAVKKYKIPLHVDAICGGLIVMEKAGYPLEHPDFRYKGVTSISADTHKKYAPBK 360
QY 361 SSVLYISDKKRRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENCYVAT 420
DB 361 SSVLYISDKKRRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENCYVAT 420
QY 421 KOITTAPELSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
DB 421 KOITTAPELSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
QY 481 PSIHFCITLLHARKKRAVLAQFLKDIRESYTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
DB 481 PSIHFCITLLHARKKRAVLAQFLKDIRESYTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 4
US-09-740-369-2
; Sequence 2, Application US/09740369
; Patent No. US20020168710A1
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID MALCOLM
; APPLICANT: GODDEN, ROBERT JAMES
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30034-D1
; CURRENT APPLICATION NUMBER: US/09/740,369
; PRIOR APPLICATION NUMBER: EP 98300625.5
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: UK 9824026.0
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; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 09/238,373
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 568
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-740-369-2

Query Match          99.4%; Score 2959; DB 10; Length 568;
Best Local Similarity 99.5%; Pred. No. 1.8e+285;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPSTDLLMLKAFEPYLEILEVYSTKAKNYVNGHCTKYPEPMOLIAWSVYVTLTIWGYEFV 60
DB 1 MPSTDLLMLKAFEPYLEILEVYSTKAKNYVNGHCTKYPEPMOLIAWSVYVTLTIWGYEFV 60
QY 61 FQPELSMRFRKKCKEKLTRKMPITIGRKIODKLNTKDDISKMSFLKVDKEYVAKLPSSQG 120
DB 61 FQPELSMRFRKKCKEKLTRKMPITIGRKIODKLNTKDDISKMSFLKVDKEYVAKLPSSQG 120
QY 121 LSSSAVLEKLEKSSMDAFMOEGRASGTIVYSGEEKLTBLVKA YGDFAMSNPLHDPDPG 180
DB 121 LSSSAVLEKLEKSSMDAFMOEGRASGTIVYSGEEKLTBLVKA YGDFAMSNPLHDPDPG 180
QY 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
DB 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
QY 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
DB 181 LKRTAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDLAFEKGITPELVAPOS 240
QY 241 AHAANKAASYFGMKIVVPLTKMMEVDVRAAMRAISRNTAMLCSTQFPHGVDPVPE 300
DB 241 AHAANKAASYFGMKIVVPLTKMMEVDVRAAMRAISRNTAMLCSTQFPHGVDPVPE 300
QY 301 VAKLAVKKYKIPLHVDAICGGLIVMEKAGYPLEHPDFRYKGVTSISADTHKKYAPBK 360
DB 301 VAKLAVKKYKIPLHVDAICGGLIVMEKAGYPLEHPDFRYKGVTSISADTHKKYAPBK 360
QY 361 SSVLYISDKKRRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENCYVAT 420
DB 361 SSVLYISDKKRRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENCYVAT 420
QY 421 KOITTAPELSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
DB 421 KOITTAPELSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
QY 481 PSIHFCITLLHARKKRAVLAQFLKDIRESYTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
DB 481 PSIHFCITLLHARKKRAVLAQFLKDIRESYTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 5
US-10-053-510-18
; Sequence 18, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrist, Henrik
; TITLE OF INVENTION: SPRINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 568
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TYPE: PR1
ORGANISM: Homo sapiens
US-10-053-510-18

Query Match
Best Local Similarity 99.4%; Score 2959; DB 12; Length 568;
Matches 565; Conservativity 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYEPWQLIAMSVVTLTIWGYEFV 60
DB 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYEPWQLIAMSVVTLTIWGYEFV 60
QY 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTDDISKNSFLKVKDEYKALPSOG 120
DB 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTDDISKNSFLKVKDEYKALPSOG 120
QY 121 LSSSAVLEKLEKXSSMDAFWQEGRASGTYSGEEKTELIVKAYGDFANSNPLHPDIFPG 180
DB 121 LSSSAVLEKLEKXSSMDAFWQEGRASGTYSGEEKTELIVKAYGDFANSNPLHPDIFPG 180
QY 181 LKRIEIVRIACSLFNGSGCGVTSIGTESILMACACRDLAFKIKTPEIYAPQS 240
DB 181 LKRIEIVRIACSLFNGSGCGVTSIGTESILMACACRDLAFKIKTPEIYAPQS 240
QY 241 AHAFAFKKASYEGMKIVRVPPLTKMEVDVRRAMRAISRNTAMLCVSTPOFPHGVIDPVE 300
DB 241 AHAFAFKKASYEGMKIVRVPPLTKMEVDVRRAMRAISRNTAMLCVSTPOFPHGVIDPVE 300
QY 301 VAKLAVKXKIPLVHVDACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKXKIPLVHVDACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSVLVYSDKKRYNYOFVDTWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
DB 361 SSVLVYSDKKRYNYOFVDTWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
QY 421 KQIKTARFLKSELENIKGFVFGNPSLIALGSRDPDIYRLSNLMTAKGNLNOLOPP 480
DB 421 KQIKTARFLKSELENIKGFVFGNPSLIALGSRDPDIYRLSNLMTAKGNLNOLOPP 480
QY 481 PSIHFCITLLHAKRRAVIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVYDRNMAVE 540
DB 481 PSIHFCITLLHAKRRAVIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVYDRNMAVE 540
QY 541 LSSVFLDSLSTDTVTYQSGOMNGSPKRP 568
DB 541 LSSVFLDSLSTDTVTYQSGOMNGSPKRP 568

RESULT 6
US-10-197-073-2
Sequence 2, Application US/10197073
Publication No. US20030166897A1
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/197, 073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Urvalter, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116, 40202
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-197-073-2

Query Match
Best Local Similarity 85.8%; Score 2553; DB 12; Length 568;
Matches 477; Conservativity 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYEPWQLIAMSVVTLTIWGYEFV 60
DB 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYEPWQLIAMSVVTLTIWGYEFV 60
QY 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTDDISKNSFLKVKDEYKALPSOG 120
DB 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTDDISKNSFLKVKDEYKALPSOG 120
QY 121 LSSSAVLEKLEKXSSMDAFWQEGRASGTYSGEEKTELIVKAYGDFANSNPLHPDIFPG 180
DB 121 LSSSAVLEKLEKXSSMDAFWQEGRASGTYSGEEKTELIVKAYGDFANSNPLHPDIFPG 180
QY 181 LKRIEIVRIACSLFNGSGCGVTSIGTESILMACACRDLAFKIKTPEIYAPQS 240
DB 181 LKRIEIVRIACSLFNGSGCGVTSIGTESILMACACRDLAFKIKTPEIYAPQS 240
QY 241 AHAFAFKKASYEGMKIVRVPPLTKMEVDVRRAMRAISRNTAMLCVSTPOFPHGVIDPVE 300
DB 241 AHAFAFKKASYEGMKIVRVPPLTKMEVDVRRAMRAISRNTAMLCVSTPOFPHGVIDPVE 300
QY 301 VAKLAVKXKIPLVHVDACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKXKIPLVHVDACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSVLVYSDKKRYNYOFVDTWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
DB 361 SSVLVYSDKKRYNYOFVDTWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
QY 421 KQIKTARFLKSELENIKGFVFGNPSLIALGSRDPDIYRLSNLMTAKGNLNOLOPP 480
DB 421 KQIKTARFLKSELENIKGFVFGNPSLIALGSRDPDIYRLSNLMTAKGNLNOLOPP 480
QY 481 PSIHFCITLLHAKRRAVIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVYDRNMAVE 540
DB 481 PSIHFCITLLHAKRRAVIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVYDRNMAVE 540
QY 541 LSSVFLDSLSTDTVTYQSGOMNGSPKRP 567
DB 541 LSSVFLDSLSTDTVTYQSGOMNGSPKRP 567

RESULT 7
US-10-053-510-6
Sequence 6, Application US/10053510
Publication No. US20030173939A1
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Fyrist, Henrik
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
POLYNUCLEOTIDES AND MODULATING AGENTS AND

TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402C2
CURRENT APPLICATION NUMBER: US/10/053.510
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 568
TYPE: PRT
ORGANISM: Mus musculus
US-10-053-510-6

Query Match 85.8%; Score 2553; DB 12; Length 568;
Best Local Similarity 84.1%; Pred. No. 4.8e-245;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPTDLMKAFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWGEFV 60
DB 1 MPTDLMKAFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWYELI 60
QY 61 FQESLSMRKKKCFKTRKMPITIGRKIDOKLTKTDISKNNSEFLKVDKEYKALPSQ 120
DB 61 FQESLSMRKKKCFKTRKMPITIGRKIDQVSKAKDLVKNMFLKVDKYKTLPAQ 120
QY 121 LSSAVLEKLEKESMDAFWQEGRASGVYSGEKTLELLVAYGDFWNSPLHPIFP 180
DB 121 MGTAEVLERKEYSSMGDSWQEGKASGAVYNGEKLLELVQAYGEFTWSNPLHPIFP 180
QY 181 LRKIEATVIRIACSLFNGGPDSCGCVTSGGTESILMACKACRDIAFEKGIKTEIVAP 240
DB 181 LRKLEATVIRIACSLFNGGPDSCGCVTSGGTESILMACKAYRDLAEKGIKTEIVAP 240
QY 241 AHAFAFNKASVFGMKIVRVPLTKMMEYDVAMBRARISRNAMLVCSPTOPHGYIDVPE 300
DB 241 AHAFAFNKASVFGMKIVRVPLTKMMEYDVAMBRARISRNAMLVCSPTOPHGYIDVPE 300
QY 301 VAKLAVYKIRPLHVDAKLGFLIVFMKAGYPLEHPDFRVKGVTSISADTHKGYAPK 360
DB 301 VAKLTVYKIRPLHVDAKLGFLIVFMKAGYPLEKPRDFRVKGVTSISADTHKGYAPK 360
QY 361 SSLVLYSDKKYRYNOFVDVDMOGGIYASPTIAGSRPGISACMAALMHFGENGYEAT 420
DB 361 SSVAVMSNEKRYRYNOFVDVDMOGGIYASPTIAGSRPGISACMAALMHFGENGYEAT 420
QY 421 KOIITKARFLKSELENKIFVFGNPLSLIAGSRPDIYRLSNLTAGWNLNOQFP 480
DB 421 KOIITKARFLKSELENKIFVFGDPLSLIAGSNDFDIYRLSNMMSAGWNNYLOFP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
DB 481 RSIHFCITLVHTKRRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQATIDRKLVAE 540
QY 541 LSSVFLDSLSTDTVTGSGOMNGSPK 567
DB 541 ISSVFLDCLYTDPTVTGOMNGSPK 567

RESULT 8
US-10-286-175-2
Sequence 2, Application US/10286175
Publication No. US2003005922A1
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/286.175
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman, Steven J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200116.402C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-286-175-2

Query Match 85.8%; Score 2553; DB 15; Length 568;
Best Local Similarity 84.1%; Pred. No. 4.8e-245;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPTDLMKAFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWGEFV 60
DB 1 MPTDLMKAFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWYELI 60
QY 61 FQESLSMRKKKCFKTRKMPITIGRKIDOKLTKTDISKNNSEFLKVDKEYKALPSQ 120
DB 61 FQESLSMRKKKCFKTRKMPITIGRKIDQVSKAKDLVKNMFLKVDKYKTLPAQ 120
QY 121 LSSAVLEKLEKESMDAFWQEGRASGVYSGEKTLELLVAYGDFWNSPLHPIFP 180
DB 121 MGTAEVLERKEYSSMGDSWQEGKASGAVYNGEKLLELVQAYGEFTWSNPLHPIFP 180
QY 181 LRKIEATVIRIACSLFNGGPDSCGCVTSGGTESILMACKACRDIAFEKGIKTEIVAP 240
DB 181 LRKLEATVIRIACSLFNGGPDSCGCVTSGGTESILMACKAYRDLAEKGIKTEIVAP 240
QY 241 AHAFAFNKASVFGMKIVRVPLTKMMEYDVAMBRARISRNAMLVCSPTOPHGYIDVPE 300
DB 241 AHAFAFNKASVFGMKIVRVPLTKMMEYDVAMBRARISRNAMLVCSPTOPHGYIDVPE 300
QY 301 VAKLAVYKIRPLHVDAKLGFLIVFMKAGYPLEHPDFRVKGVTSISADTHKGYAPK 360
DB 301 VAKLTVYKIRPLHVDAKLGFLIVFMKAGYPLEKPRDFRVKGVTSISADTHKGYAPK 360
QY 361 SSLVLYSDKKYRYNOFVDVDMOGGIYASPTIAGSRPGISACMAALMHFGENGYEAT 420
DB 361 SSVAVMSNEKRYRYNOFVDVDMOGGIYASPTIAGSRPGISACMAALMHFGENGYEAT 420
QY 421 KOIITKARFLKSELENKIFVFGNPLSLIAGSRPDIYRLSNLTAGWNLNOQFP 480
DB 421 KOIITKARFLKSELENKIFVFGDPLSLIAGSNDFDIYRLSNMMSAGWNNYLOFP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
DB 481 RSIHFCITLVHTKRRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQATIDRKLVAE 540
QY 541 LSSVFLDSLSTDTVTGSGOMNGSPK 567
DB 541 ISSVFLDCLYTDPTVTGOMNGSPK 567

RESULT 9

US-10-197-073-10
: Sequence 10, Application US/10197073
: Publication No. US20030166897A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed Intellectual Property Law Group
: STREET: 701 Fifth Avenue, Suite 6300
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98055
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/197,073
: FILING DATE: 15-Jul-2002
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Urvater, Julie A.
: REGISTRATION NUMBER: 50,461
: REFERENCE/DOCKET NUMBER: 200116,402D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 488 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-197-073-10

Query Match 83.9%; Score 2498; DB 12; Length 488;
Best Local Similarity 85.9%; Pred. No. 1,le-239;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;
DB 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIIVGGEFV 60
1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIIVGGEFV 60
QY 61 FQPELSMSRFKKCKRKLTKRMPITGRKIODKLNKT KDISKMSFLKYDKEYVKALPSQG 120
61 FQPELSMSRFKKCKRKLTKRMPITGRKIODKLNKT KDISKMSFLKYDKEYVKALPSQG 120
DB 121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
QY 181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
DB 181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
QY 241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
DB 241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
QY 301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
DB 301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
QY 361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
DB 361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420

RESULT 10
US-10-053-510-10
: Sequence 10, Application US/10053510
: Publication No. US20030175939A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Applicant: Fyfe, Henrik
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
: POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: FILE REFERENCE: 200116,402C2
: CURRENT APPLICATION NUMBER: US/10/053,510
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 488
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-053-510-10

Query Match 83.9%; Score 2498; DB 12; Length 488;
Best Local Similarity 85.9%; Pred. No. 1,le-239;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;
DB 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIIVGGEFV 60
1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIIVGGEFV 60
QY 61 FQPELSMSRFKKCKRKLTKRMPITGRKIODKLNKT KDISKMSFLKYDKEYVKALPSQG 120
61 FQPELSMSRFKKCKRKLTKRMPITGRKIODKLNKT KDISKMSFLKYDKEYVKALPSQG 120
DB 61 FQPELSMSRFKKCKRKLTKRMPITGRKIODKLNKT KDISKMSFLKYDKEYVKALPSQG 120
61 FQPELSMSRFKKCKRKLTKRMPITGRKIODKLNKT KDISKMSFLKYDKEYVKALPSQG 120
QY 121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
DB 121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
QY 181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
DB 181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
181 LKRIAEIYRIACSLFNGPDSGCVTSGGTESIIMACKACHDLAFEGKIKTPEIYAPQS 240
QY 241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
DB 241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
241 AHAANAKAAYFGMKIVRPLTKMMEVDVRAARRAISRTAMLCVSTPOFPHGVIDPYPE 300
QY 301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
DB 301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
301 VAKLAVKKIPLHVACAGGLIVFMERAGYPLEHPDFRKYGVTSISADTHK 360
QY 361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
DB 361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
361 SSLVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISAAWALMHFGENGVEAT 420
QY 421 KOITKAPFLKSELENIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNLQLOPP 480
421 KOITKAPFLKSELENIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNLQLOPP 480
DB 421 KOITKAPFLKSELENIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNLQLOPP 480
421 KOITKAPFLKSELENIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNLQLOPP 480
QY 481 PSIHFCITLLHARKKRAIOLFIDRESYQIKNPKAKTTGGAITYAMAQTTVDNRMAVE 540
481 PSIHFCITLLHARKKRAIOLFIDRESYQIKNPKAKTTGGAITYAMAQTTVDNRMAVE 540
DB 481 PSIHFCITLLHARKKRAIOLFIDRESYQIKNPKAKTTGGAITYAMAQTTVDNRMAVE 540
481 PSIHFCITLLHARKKRAIOLFIDRESYQIKNPKAKTTGGAITYAMAQTTVDNRMAVE 540

Db 401 PSIHFCITLLHARRKRAIOFLKDIRESVTOIMKNPKAKTTGMAIYMAOQTVDRNNVAE 460
QY 541 LSSVFLDSLXSTDTVTGSGOMNSPKPH 568
Db 461 LSSVFLDSLXSTDTVTGSGOMNSPKPH 488

RESULT 11
US-10-286-175-10
: Sequence 10, Application US/10286175
: Publication No. US2003005922A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed Intellectual Property Law Group
: STREET: 701 Fifth Avenue, Suite 6300
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98055
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/286.175
: FILING DATE: 30-Oct-2002
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Roseman, Steven J.
: REGISTRATION NUMBER: 43,058
: REFERENCE/DOCKET NUMBER: 200116.402C3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 662-6031
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 488 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-286-175-10

Query Match 83.9%; Score 2498; DB 15; Length 488;
Best Local Similarity 85.9%; Pred. No. 1,1e-239;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MPSTDLMLKAFEPYILEVYSTKAKNYNGHCTKYEPMOLIAMSVYVMTLLIYMGYEFV 60
Db 1 MPSTDLMLKAFEPYILEVYSTKAKNYNGHCTKYEPMOLIAMSVYVMTLLIYMGYEFV 60
QY 61 FQPESLMSRRKKCKFKLTRKMPITIGRIQDKLNTKDDISKNSFLKVDREYVAKLPDSOG 120
Db 61 FQPESLMSRRKKCKFKLTRKMPITIGRIQDKLNTKDDISKNSFLKVDREYVAKLPDSOG 120
QY 121 LSSSAVLEKLEKYSMAFQEGRASTGVSGEKLTELLYKAYGDPANSNPLHDPFPG 180
Db 121 LSSSAVLEKLEKYSMAFQEGRASTGVSGEKLTELLYKAYGDPANSNPLHDPFPG 180
QY 181 LRKIEAIVRIACSLFNGCPDSCGCVSGTSTILMACACRDIAFEKGIKTPETIVAPQS 240
Db 181 LRKIEAIVRIACSLFNGCPDSCGCVSGTSTILMACACRDIAFEKGIKTPETIVAPQS 240
QY 241 AHAFAFNKAASTFGKIVRVPILTKMEVDVVRAMRAISRNTAMLVCSPTQEPHGVDPPE 300
Db 241 AHAFAFNKAASTFGKIVRVPILTKMEVDVVRAMRAISRNTAMLVCSPTQEPHGVDPPE 300

QY 301 VAKLAVKYPILPHVDAICGFLIVFMERKAGYPLEHPDFRKGVTSISADTHKYGAPKG 360
Db 301 VAKLAVKYPILPHVDAICGFLIVFMERKAGYPLEHPDFRKGVTSISADTHK 353
QY 361 SSLVYSDDKRYNRYOFFVDTDWOGIYASPTIAGSRPGISAACMAALMHFGENGVEAT 420
Db 361 353
QY 421 KQIITKARFLKSELENKIGFVGNPQLSLIAGSRPDIYRSLNLTAKGWLNOQFP 480
Db 421 400
QY 481 PSIHFCITLLHARRKRAIOFLKDIRESVTOIMKNPKAKTTGMAIYMAOQTVDRNNVAE 540
Db 401 PSIHFCITLLHARRKRAIOFLKDIRESVTOIMKNPKAKTTGMAIYMAOQTVDRNNVAE 460

QY 541 LSSVFLDSLXSTDTVTGSGOMNSPKPH 568
Db 461 LSSVFLDSLXSTDTVTGSGOMNSPKPH 488

RESULT 12
US-10-053-510-16
: Sequence 16, Application US/10053510
: Publication No. US20030175939A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Fyset, Henrik
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
: POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: FILE REFERENCE: 200116.402C2
: CURRENT APPLICATION NUMBER: US/10/053.510
: CURRENT FILING DATE: 2002-01-17
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 16
: LENGTH: 545
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-10-053-510-16

Query Match 45.1%; Score 1344; DB 12; Length 545;
Best Local Similarity 49.0%; Pred. No. 1,1e-124;
Matches 254; Conservative 100; Mismatches 160; Indels 4; Gaps 4;

QY 38 EPMOLIAMSVYVMTLLIYMGYEFVQPELSMRKKCKFKLTRKMPITIGRIQDKLNTKTD 97
Db 25 EPMQVATITATVTYLVGVMWMTVTCQDENLIRGRQFFKPAKIPAVRQVETELAKKN 84
QY 98 DISKNSFLKVDREYVAKLPDSOGIASSAVLEKLEKYSMDAF-WQEGRASGVYSGEKL 156
Db 85 DPEIEIKKSNNAHLITSETLPEKGSKEEILRLVDEHLKTHGYNWRDRAVSGAVGYKPD 144
QY 157 TELLYKAYGDPANSNPLHDPFPGRLKIEAIVRIACSLFNGCPDSCGCVSGTSTILM 216
Db 145 VELTVEYGRASVTNPLHADLPFCVCKMEAEVVRMAACNLHGNSASCGTMTGTGTESTIVM 204
QY 217 ACKACRDIAFE-KGIRKPEIIVAPQSAHAANAKASYGKIVRPL-TKMEVDVVRAMR 274
Db 205 AMKAYRDFAREYKGITRPNIVPRTVHAADKGGQYFNHIVRSVDVPEYEVDIKKFKR 264
QY 275 AISRNTAMLVCSPTQEPHGVIDPVYVAKLAVKYPILPHVDAICGFLIVFMERKAGYPLE 334
Db 265 AINRNTILVGSAPNPFYGTIDIDEAIAAGVYVDIPVHVDAICGSFVALVHNAGKYL- 323
QY 335 HPDFRKYGVTSISADTHKYGAPKGSLLVYSDDKRYNRYOFFVDTDWOGIYASPTIAG 394
Db 324 RPDEYKGVTSISADTHKYGAPKGSLLVYSDDKTKDQFYTTDMPGCVGSGSPVNG 383
QY 395 SRPGISAACMAALMHFGENGVEATKQIITKARFLKSELENKIGFVGNPQLSLIAG 454
Db 395 454

Db 384 SAGGIIACGATMMSFGDGLTEATKRVDTARIENGVDIDGIFFGPATSVIALG 443
Qy 455 SRDPDIYRLSNLTAKGNLNLQLOPPPSIHFCITLLHAKRYAIOFLKDIREVTOIMKN 514
Db 444 SVPDFIFRLSDSLCKLGNMLNLQPPSGHLCVDMHNPQGVADFIADVRCSTAEIMKD 503
Qy 515 PRAKTTGCAITAAQTTVDNRMMVAELSVFLDSLXT 552
Db 504 PCQPVYGMKALYGAQSIPIRDSVIGEVTRLFLHSMYTT 541

RESULT 13

US-10-053-510-11
; Sequence 11, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyfe, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053, 510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 552
; TYPE: PRT
; ORGANISM: C. elegans
US-10-053-510-11

Query Match 36.3%; Score 1082; DB 12; Length 552;
Best Local Similarity 42.7%; Pred. No. 1.4e-98;
Matches 228; Conservative 97; Mismatches 197; Indels 12; Gaps 7;

Qy 30 VNGHCTKYEPNOLI-----AMSVYVTLILYMGIEPVFPQPSLSMRKKKCFKLTAKPITG 85
Db 22 INDRLSRYDPPVYLAAFGGLVYTKV---HLRYKSEDPILKRMGAVYFSLRLKLPAYR 78
Qy 86 RKIOPKLNKTKDISKNSFLKVDKEYKALPSSGSSAVLEKKEYSMDAF-WQEGR 144
Db 79 DKIEKELAEKPKLIESIKDKDKOFISTLPRIAPLSQDSIMELAKKIYEDYTFNIDGR 138
Qy 145 ASGTVYSGEE-KLTLLVYKAYGDFAMSNPLHPDIFPGRLKRIEATVIRIACSLFNGSPSC 203
Db 139 VSGAVYTDHNAHINLIGIKIYKAFSNPLHPDVPFGAKMEALIRVNLINYPEDSS 198
Qy 204 GCVTSGGTSSILMAKACDLAFEGKIKTPEIYVAPQSAHAFAFNKAASYFGMKIVRPLTK 263
Db 199 GSVTSGGTSSILMAFGSYRNRAHSLGIEHPVILACKTAHAADFKAHLGCMELRHVPVDS 258
Qy 264 KMEVDVRAAMRAISRNTAMLCSTPOFPHGVIDPVEVAKLVAKYKIPLVHVDACLGFLI 323
Db 259 DNRVLDKEKMERLIDSNVCLVGSAPNFPSTGIDPRLPIAKLKGKIGIPIVHVDACLGFLI 318
Qy 324 VMEKAGYPLEHPDFEFKVGYSISADTHKYGVARPGSSLVLYSDKKYRNYOFVDTMQ 383
Db 319 PEMNADGY-LIIPVDFERNPGVYSISCDTHKYGCTPKGSSIVMYRSKELHHFQYFSVADMC 377
Qy 384 GGIVASPTIAGSRPGISACMAALMHFENGVEYVETKQITKARFLKSELNINIGIYF 443
Db 378 GGIVASPTIAGSRAGANTAVAMATLLSFGREDEYVRCQAQIVKTRMLAKRIKIKIRY 437
Qy 444 GNPOSLIALGSRDPIYRLSNLTAKGNLNLQLOPPPSIHFCITLLHAKRYAIOFLKD 503
Db 438 GNSDVSIVAFSGNGVNIYVSDKMKLGNMLNTLONPAIHICTITINQANEVVAFAVD 497
Qy 504 IRESVTQI-MKNPKAKTTGGAIVAAQTTVDNRMMVAELSVFLDSLXTDTVT 556
Db 498 LEKICEELAAKGEOQKADSGMAAMYGA-AQVPKSVYDEVIALIYDATYSAPST 550

RESULT 14

US-10-197-073-6
; Sequence 6, Application US/10197073
; Publication No. US20030166897A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197,073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Urvalter, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116.402D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-197-073-6

Query Match 33.9%; Score 1008; DB 12; Length 542;
Best Local Similarity 38.1%; Pred. No. 3.2e-91;
Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

Qy 19 LEVYSTKAKNRYNGCHCTYEPNOLIAMSVMYVTLILYMGIEPVFPQPSLSMRKKKCFKLT 78
Db 5 LEQYHS-ABDLIFELRKFNPVLVSTIVATVYVLTNLRHMLHDEMGRKRLSTWFFTTV 63
Qy 79 RKPPIIGRKIOPKLNKTKDISKNSFLKVDKEYKALPSSGSSAVLEKKEYSMDA 138
Db 64 KRVPIIRKIMDKQLNMEVDELEKSLRIYDRSTREYFTTIPSHSVGRTVRLAIAIYDDLEG 123
Qy 139 -FWQGRASGTVYSGEELK--TELLVYKAYGDFAMSNPLHPDIFPGRLKRIEATVIRIACSL 195
Db 124 PAFLEGKSGVAGFVNEDEKDEREMEYEVGFAMNPMPKLPFGVRIIMEAEVVMCCNM 183
Qy 196 FMGPGDSCGVTSGGTSSILMAKACDLAFEGKIKTPEIYVAPQSAHAFAFNKAASYFGMK 255
Db 184 MNGDSETCGMSTGSSISILCLAHNRNLKRGKRYEMAYPVSSVHAAFKAAACCFRIK 243
Qy 256 IYRVPPLTKM-MEVDVRAAMRAISRNTAMLCSTPOFPHGVIDPVEVAKLVAKYKIPLVH 314
Db 244 VKRIIVDPVTFKVDLVKKAAINRKTCLVGSAPNFPSTGIDPRLPIAKLKGKIGIPIVHVD 303
Qy 315 DACLGGLIVMEKAGYPLEHPDFEFKVGYSISADTHKYGVARPGSSLVLYSDKKYRNY 374
Db 304 DACLGGLFLPELEED-----EIRYDRIYVPGVSSISADSHKYGVARPGSSLVLYRNNELAHN 359
Qy 375 QFVVDTDQGGIYASPTIAGSRPGISACMAALMHFENGVEYVETKQITKARFLKSEL 434

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QY      435 ENIKGIFVFGNPNQSLIALGSRD-FDIYRLSNLTAKGWNLNQOPPSIHFCITLLHAR 493
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Db      420 SNIKGILQGPSDVCIYSWTNDGVELYRFHNFMEKEKHQNLQGFAGVHIMVTMNH 479
QY      494 KRAVIOFLKDIRESVTQIM--KNPKAKTTGGAITYAMAQTTVDNRNVAELSSVFLDSL 551
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US-10-053-510-4
; Sequence 4, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Eyrst, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: C. elegans
US-10-053-510-4
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Query Match 33.9%; Score 1008; DB 12; Length 542;

Best Local Similarity 38.1%; Pred. No. 3.2e-91;

Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

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QY      196 FNGPDCGCVTSQGTESIIMACACRDLAFKGIKTPETIYAPQSAHAFAFNKASVFGMK 255
        | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
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QY      256 IYRVPLTKM-MEVDYRAMRRAISNTAMLYCSTPQPHGVIDPYVEVAKLAVKYIPLHV 314
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Db      244 VRKIPVDVPEFKVDLVKMKAIKRTCLVGSAPNPEGTVDIEAIGQLGEVDIPVHV 303
QY      315 DACIGGLIYMEKAGYPLEHPEFPRYKGYTISADTHKKYGAAPKGSVLVYSDKRYNY 374
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Db      360 QYFCDDADMOGCIYASATMEGSRAGHNIALCWAAMLHYAQBEGYKANARKIYDTTRKIRNGL 419
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QY      494 KRAVIOFLKDIRESVTQIM--KNPKAKTTGGAITYAMAQTTVDNRNVAELSSVFLDSL 551
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Search completed: October 6, 2003, 13:57:16
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 13:46:54 ; Search time 25 seconds

(without alignments)
961.303 Million cell updates/sec

Title: US-10-053-510-8

Perfect score: 2977
Sequence: 1 MPSTDLLMLKAFPEYLEILE.....LYSDRYTQGSQMNQSPKPH 568

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2977	100.0	568	US-08-939-309-4	Sequence 4, Appli
2	2977	100.0	568	US-09-849-180-4	Sequence 4, Appli
3	2977	100.0	568	US-09-356-643B-8	Sequence 8, Appli
4	2959	99.4	568	US-09-238-373-2	Sequence 2, Appli
5	2959	99.4	568	US-09-740-369-2	Sequence 2, Appli
6	2553	85.8	568	US-08-939-309-2	Sequence 2, Appli
7	2553	85.8	568	US-09-849-180-2	Sequence 2, Appli
8	2553	85.8	568	US-09-356-643B-6	Sequence 6, Appli
9	2498	83.9	488	US-08-939-309-10	Sequence 10, Appli
10	2498	83.9	488	US-09-849-180-10	Sequence 10, Appli
11	2498	83.9	488	US-09-356-643B-10	Sequence 10, Appli
12	1082	36.3	552	US-09-356-643B-11	Sequence 11, Appli
13	1008	33.9	542	US-08-939-309-6	Sequence 6, Appli
14	1008	33.9	542	US-09-849-180-6	Sequence 6, Appli
15	1008	33.9	542	US-09-356-643B-4	Sequence 4, Appli
16	1007.5	33.8	589	US-08-939-309-8	Sequence 8, Appli
17	1007.5	33.8	589	US-09-849-180-8	Sequence 8, Appli
18	1007.5	33.8	589	US-09-356-643B-2	Sequence 2, Appli
19	355	11.9	76	US-09-238-373-4	Sequence 4, Appli
20	355	11.9	76	US-09-740-369-4	Sequence 4, Appli
21	258.5	8.7	466	US-09-068-195-25	Sequence 25, Appli
22	194	6.5	525	US-09-328-352-4492	Sequence 4492, Ap
23	155.5	5.2	502	US-09-134-001C-3598	Sequence 3598, Ap
24	148.5	5.0	489	US-09-134-001C-2920	Sequence 2920, Ap
25	144.5	4.9	398	US-09-328-352-4507	Sequence 4507, Ap
26	144	4.8	393	US-09-377-557-14	Sequence 14, Appli
27	137	4.6	583	5475086-4	Patent No. 5475086

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29	131	4.4	584	2	US-08-450-755-1	Sequence 2, Appli
30	131	4.4	585	1	US-08-117-907-2	Sequence 1, Appli
31	131	4.4	585	1	US-08-485-718-11	Sequence 11, Appli
32	131	4.4	585	1	US-08-485-718-13	Sequence 13, Appli
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37	131	4.4	585	2	US-08-827-618A-57	Sequence 57, Appli
38	131	4.4	585	2	US-08-827-618A-57	Sequence 57, Appli
39	131	4.4	585	3	US-08-483-952A-57	Sequence 57, Appli
40	131	4.4	585	3	US-08-483-952A-59	Sequence 59, Appli
41	131	4.4	585	4	US-08-453-040-2	Sequence 2, Appli
42	131	4.4	585	4	US-08-476-501-57	Sequence 57, Appli
43	128	4.3	585	3	US-08-476-501-59	Sequence 59, Appli
44	128	4.3	585	3	US-09-043-930-5	Sequence 5, Appli
45	127.5	4.3	585	6	5475086-6	Patent No. 5475086
			466	4	US-09-107-532A-4022	Sequence 4022, Ap

ALIGNMENTS

RESULT 1
US-08-939-309-4
; Sequence 4, Application US/08939309

; Patent No. 6423527

GENERAL INFORMATION:
APPLICANT: Saba, Julie D.

APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SPIRINOSINE-1-PHOSPHATE LYASE

TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Query Match 100.0%; Score 2977; DB 4; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,7e-279;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTDLLMLKAFPEYLEILEYSTRKAKYVNGHCKTKYEPWOLIANSVYVTLIIWGYEFV 60
DB 1 MPSTDLLMLKAFPEYLEILEYSTRKAKYVNGHCKTKYEPWOLIANSVYVTLIIWGYEFV 60

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QY 61 PPESTMSRFRKKCFKLTTRKMPITGRKIDDKLTKDDISKNNMFLKVDKEYKALPSOG 120
DB 61 PPESTMSRFRKKCFKLTTRKMPITGRKIDDKLTKDDISKNNMFLKVDKEYKALPSOG 120
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DB 121 LSSSAVLEKLEKESMDAFWQEGRASGYVSGEEKLTLLVAYGDFAMSNPLHPDIFPG 180
QY 181 LKRIEAEIVRIACSLFNGSPDSCGCVTSGGTESIIMACACRDLAEKGIKTPETIAPOS 240
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QY 241 AHAFAFKASGYGKIVRPLTKMMEVDVRAAMRAISRNTAMLCSTPQFPBGVIDPVE 300
DB 241 AHAFAFKASGYGKIVRPLTKMMEVDVRAAMRAISRNTAMLCSTPQFPBGVIDPVE 300
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DB 301 VAKLAVKYPILPHVDACLGFLIVMEKAGYPLEHFPDRVKGVSISADTHKYGAPRG 360
QY 361 SSLVLYSDKKYNNYQFVDTMOGGIYASPTIAGSRPGISACWMAALMHFGENGVEAT 420
DB 361 SSLVLYSDKKYNNYQFVDTMOGGIYASPTIAGSRPGISACWMAALMHFGENGVEAT 420
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DB 421 KOIITARFLKSELENIKIFVFGNPOSLIALGSRDPDIYRLSNLMTAKGNLNOLOPP 480
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DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 2
US-09-849-180-4
; Sequence 4, Application US/09849180
; Patent No. 6495359
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98055
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,180
; FILING DATE: 04-May-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pepe, Jeffrey C.
; REGISTRATION NUMBER: 46,985
; REFERENCE/DOCKET NUMBER: 200116, 402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-849-180-4

Query Match      100.0%; Score 2977; DB 4; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,7e-279;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTDLLMKAPPEYLELEVSTKAKNVNCHCTKYEPMQILAMSVVMTLLIVMGYEV 60
DB 1 MPSTDLLMKAPPEYLELEVSTKAKNVNCHCTKYEPMQILAMSVVMTLLIVMGYEV 60
QY 61 PPESTMSRFRKKCFKLTTRKMPITGRKIDDKLTKDDISKNNMFLKVDKEYKALPSOG 120
DB 61 PPESTMSRFRKKCFKLTTRKMPITGRKIDDKLTKDDISKNNMFLKVDKEYKALPSOG 120
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DB 121 LSSSAVLEKLEKESMDAFWQEGRASGYVSGEEKLTLLVAYGDFAMSNPLHPDIFPG 180
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DB 241 AHAFAFKASGYGKIVRPLTKMMEVDVRAAMRAISRNTAMLCSTPQFPBGVIDPVE 300
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DB 421 KOIITARFLKSELENIKIFVFGNPOSLIALGSRDPDIYRLSNLMTAKGNLNOLOPP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPKAKTTGGAITYAMAQTTVDNRMAE 540
DB 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPKAKTTGGAITYAMAQTTVDNRMAE 540
QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 3
US-09-356-643B-8
; Sequence 8, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 200116, 402C1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-356-643B-8

Query Match      100.0%; Score 2977; DB 4; Length 568;

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Best Local Similarity 100.0%; Pred. No. 2,7e-279;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPSTDLMLKAFEEYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60
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Db 61 FQPELSLRFKKKCFKTLRKMPITIGRKIODKLNKTODISKNSMFLKVDKRYVALPSQG 120
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Db 121 LSSSAVLEKLEYSMDAFMOEGRASGVYSGEEKTELKAYKAGDFAMSNPLHPDIFPG 180
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Db 181 LRKTEAIVRIACSLFNGGPDSCGCVTSGTESTILMACACRDIAFEKGIKTPETIVAPQS 240
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Db 301 VAKLAIVKXKIPLHVDAICLGFLIVFMEKAGYPLEHPDFRVKGYTSSADTHKKGYAPKG 360
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Db 361 SSLVLYSDKKYRNQFVDTDMOGGIYASPTIAGSRPGISAAACWALMHFGENGVEAT 420
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QY 421 KOIKTARFLKSELENKIGIFVFNPSQLSLALSGRPDIYRLSNLMTAKMWNLOLFP 480
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Db 421 KOIKTARFLKSELENKIGIFVFNPSQLSLALSGRPDIYRLSNLMTAKMWNLOLFP 480
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QY 481 PSIHFCITLLHARRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
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Db 481 PSIHFCITLLHARRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
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Db 541 LSSVFLDSLSTDTVTGSGQMNNGSPKPH 568
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RESULT 4

US-09-238-373-2
; Sequence 2, Application US/09238373A
; Patent No. 6187562
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID MALCOLM
; APPLICANT: GODDEN, ROBERT JAMES
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30034
; CURRENT APPLICATION NUMBER: US/09/238, 373A
; CURRENT FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: UK 9824026.0
; EARLIER FILING DATE: 1998-11-03
; EARLIER APPLICATION NUMBER: EP 98300625.5
; EARLIER FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-238-373-2

Query Match 99.4%; Score 2959; DB 3; Length 568;
Best Local Similarity 99.5%; Pred. No. 1.5e-277;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEEYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60

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Db 1 MPSTDLMLKAFEEYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60
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QY 61 FQPELSLRFKKKCFKTLRKMPITIGRKIODKLNKTODISKNSMFLKVDKRYVALPSQG 120
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Db 61 FQPELSLRFKKKCFKTLRKMPITIGRKIODKLNKTODISKNSMFLKVDKRYVALPSQG 120
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QY 121 LSSSAVLEKLEYSMDAFMOEGRASGVYSGEEKTELKAYKAGDFAMSNPLHPDIFPG 180
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Db 121 LSSSAVLEKLEYSMDAFMOEGRASGVYSGEEKTELKAYKAGDFAMSNPLHPDIFPG 180
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QY 181 LRKTEAIVRIACSLFNGGPDSCGCVTSGTESTILMACACRDIAFEKGIKTPETIVAPQS 240
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Db 181 LRKTEAIVRIACSLFNGGPDSCGCVTSGTESTILMACACRDIAFEKGIKTPETIVAPQS 240
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QY 241 AHAFAFNKAASYFGMKIVRVPLTKMMEVDVRRAMRAISRNTAMLCSTPQPFHGYIDPVE 300
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Db 241 AHAFAFNKAASYFGMKIVRVPLTKMMEVDVRRAMRAISRNTAMLCSTPQPFHGYIDPVE 300
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QY 301 VAKLAIVKXKIPLHVDAICLGFLIVFMEKAGYPLEHPDFRVKGYTSSADTHKKGYAPKG 360
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Db 301 VAKLAIVKXKIPLHVDAICLGFLIVFMEKAGYPLEHPDFRVKGYTSSADTHKKGYAPKG 360
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QY 361 SSLVLYSDKKYRNQFVDTDMOGGIYASPTIAGSRPGISAAACWALMHFGENGVEAT 420
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Db 361 SSLVLYSDKKYRNQFVDTDMOGGIYASPTIAGSRPGISAAACWALMHFGENGVEAT 420
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QY 421 KOIKTARFLKSELENKIGIFVFNPSQLSLALSGRPDIYRLSNLMTAKMWNLOLFP 480
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Db 421 KOIKTARFLKSELENKIGIFVFNPSQLSLALSGRPDIYRLSNLMTAKMWNLOLFP 480
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QY 481 PSIHFCITLLHARRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
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Db 481 PSIHFCITLLHARRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
    |||||||
QY 541 LSSVFLDSLSTDTVTGSGQMNNGSPKPH 568
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Db 541 LSSVFLDSLSTDTVTGSGQMNNGSPKPH 568
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RESULT 5

US-09-740-369-2
; Sequence 2, Application US/09740369
; Patent No. 6521437
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID MALCOLM
; APPLICANT: GODDEN, ROBERT JAMES
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30034-D1
; CURRENT APPLICATION NUMBER: US/09/740, 369
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: EP 98300625.5
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: UK 9824026.0
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 09/238, 373
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 568
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-740-369-2

Query Match 99.4%; Score 2959; DB 4; Length 568;
Best Local Similarity 99.5%; Pred. No. 1.5e-277;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEEYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60

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OY 61 FQPSLMSRFKKCKELTRKMPITGRKIDKLNKTKDDISKNMSEFLKYDKEYVKA1PSQG 120
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DB 61 FQPSLMSRFKKCKELTRKMPITGRKIDKLNKTKDDISKNMSEFLKYDKEYVKA1PSQG 120
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OY 121 LSSAVLELKEKYESMDAFWQGRASGVYSGEEKLTLLVKAAYGDFAMSNPLHDPDIPG 180
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;
;
DB 121 LSSAVLELKEKYESMDAFWQGRASGVYSGEEKLTLLVKAAYGDFAMSNPLHDPDIPG 180
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OY 181 LKRIAEIVRIACSLFNGSPDSCGCVTSGGTESIIMACKACHDLAFKGIKTPETIYAPQS 240
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DB 181 LKRIAEIVRIACSLFNGSPDSCGCVTSGGTESIIMACKACHDLAFKGIKTPETIYAPQS 240
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OY 241 AHAENKAASYFGMKIVRPLTKMMEVDVRAIRRAISRNTAMLCSTPQPHGVDPDYPE 300
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;
;
DB 241 AHAENKAASYFGMKIVRPLTKMMEVDVRAIRRAISRNTAMLCSTPQPHGVDPDYPE 300
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OY 301 VAKLAVKKRIPLHVADCLGGLIIVMEKAGYPLEHPDFRKGVSISADTHKYGAPRG 360
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DB 301 VAKLAVKKRIPLHVADCLGGLIIVMEKAGYPLEHPDFRKGVSISADTHKYGAPRG 360
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OY 361 SLVLYSKKYRNYQFVDTDMQGGIYASPTIAGSRPGISACNAALMHFEGENGYEAT 420
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DB 361 SLVLYSKKYRNYQFVDTDMQGGIYASPTIAGSRPGISACNAALMHFEGENGYEAT 420
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OY 421 KOIKTARFLKSELENIKIFVFGNPOLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
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DB 421 KOIKTARFLKSELENIKIFVFGNPOLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
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OY 481 PSIHFCITLLHARKRVAIOFLKDIRESVQIKNKRAKTGTGALYMAQTTVDNRMAE 540
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DB 481 PSIHFCITLLHARKRVAIOFLKDIRESVQIKNKRAKTGTGALYMAQTTVDNRMAE 540
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OY 541 LSSVFLDSLSTDTVTOGSGOMNGSPKPH 568
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DB 541 LSSVFLDSLSTDTVTOGSGOMNGSPKPH 568
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RESULT 6
US-08-939-309-2
; Sequence 2, Application US/08939309
; Patent No. 6423527
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,309
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, MAKI J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 200116.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:

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;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 568 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
US-08-939-309-2
;
Query Match 85.8%; Score 2553; DB 4; length 568;
Best Local Similarity 84.1%; Pred. No. 36-238;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;
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OY 1 MPSTLLMKAFEPYLELLEVSTKAKNVNCHCTKYEPMOLIANSVWTLIIWGYEYV 60
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DB 1 MPSTLLMKAFEPYLELLEVSTKAKNVNCHCTKYEPMOLIANSVWTLIIWGYEYV 60
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DB 61 FQPSLMSRFKKCKELTRKMPITGRKIDKLNKTKDDISKNMSEFLKYDKEYVKA1PSQG 120
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DB 121 LSSAVLELKEKYESMDAFWQGRASGVYSGEEKLTLLVKAAYGDFAMSNPLHDPDIPG 180
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OY 181 LKRIAEIVRIACSLFNGSPDSCGCVTSGGTESIIMACKACHDLAFKGIKTPETIYAPQS 240
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DB 181 LKRIAEIVRIACSLFNGSPDSCGCVTSGGTESIIMACKACHDLAFKGIKTPETIYAPQS 240
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OY 241 AHAENKAASYFGMKIVRPLTKMMEVDVRAIRRAISRNTAMLCSTPQPHGVDPDYPE 300
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DB 241 AHAENKAASYFGMKIVRPLTKMMEVDVRAIRRAISRNTAMLCSTPQPHGVDPDYPE 300
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OY 301 VAKLAVKKRIPLHVADCLGGLIIVMEKAGYPLEHPDFRKGVSISADTHKYGAPRG 360
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DB 301 VAKLAVKKRIPLHVADCLGGLIIVMEKAGYPLEHPDFRKGVSISADTHKYGAPRG 360
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OY 361 SLVLYSKKYRNYQFVDTDMQGGIYASPTIAGSRPGISACNAALMHFEGENGYEAT 420
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DB 361 SLVLYSKKYRNYQFVDTDMQGGIYASPTIAGSRPGISACNAALMHFEGENGYEAT 420
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OY 421 KOIKTARFLKSELENIKIFVFGNPOLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
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DB 421 KOIKTARFLKSELENIKIFVFGNPOLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
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OY 481 PSIHFCITLLHARKRVAIOFLKDIRESVQIKNKRAKTGTGALYMAQTTVDNRMAE 540
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DB 481 PSIHFCITLLHARKRVAIOFLKDIRESVQIKNKRAKTGTGALYMAQTTVDNRMAE 540
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OY 541 LSSVFLDSLSTDTVTOGSGOMNGSPKPH 567
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DB 541 LSSVFLDSLSTDTVTOGSGOMNGSPKPH 567
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RESULT 7
US-09-849-180-2
; Sequence 2, Application US/09849180
; Patent No. 649359
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98055
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-849-180-2

Query Match 85.8%; Score 2553; DB 4; Length 568;
Best Local Similarity 84.1%; Pred. No. 3e-238;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAPFPEYLEIEVYSTKAKNYNGHCTKTEPQOLAMSVVTLTVMGYEFV 60
DB 1 MPSTDLMLKDFPEYLEIEVYSTKAKNYNGCTKTEPQOLAMSVLTLTVWYELI 60
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DB 61 FQESLSMRKKKFLFKIRKMPFIRGRIEQVSKAKKDLVKNMPLKVDYKTLPAOG 120
QY 121 LSSAVLEKIKETSSMDAFQEGRASGVYSGEKKLTLLVYKAYGDPFAMNPLHPIFP 180
DB 121 MGTAELERLEKESYSDMGQEGKASGAVYNGEPKLTLLVQAYGETWSPNPLHPIFP 180
QY 181 LRKLEIYVMTCSLFGNGDSCGCVTSGSTESILMACRACRDLAFKGIKTEPIVAP 240
DB 181 LRKLEIYVMTCSLFGNGDSCGCVTSGSTESILMACRACRDLAFKGIKTEPIVAP 240
QY 241 AHAFAKKAHYFGMKIVRPLTKMEVDVAMRRATSRNTAMLCSTPQPHGVMDVPE 300
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DB 301 VAKLAVKYYKIPLVNDAICLGGFLVFMKAGYPLEHPDFRVKGVTSISADTHKYGAP 360
QY 361 SSVLVSDKKRYNOFFVDMDGGIYASPTISGSPRGISACMAALMHFGNGYEAT 420
DB 361 SSVLVSDKKRYNOFFVDMDGGIYASPTISGSPRGISACMAALMHFGNGYEAT 420
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DB 421 KQIKTARFLKSELENIKIFVGNPOLSLIALGSDFDIYRLSNLTAKGWLNOLOFP 480
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DB 481 PSIHFCITLLHAKRVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNVAE 540
QY 541 LSSVFLDSLYSTDTVTOGSONGSPKP 567
DB 541 LSSVFLDSLYSTDTVTOGSONGSPKP 567

RESULT 8
US-09-356-643B-6
; Sequence 6, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.

TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402C1
CURRENT APPLICATION NUMBER: US/09/356,643B
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 568
TYPE: PRT
ORGANISM: Mus musculus
US-09-356-643B-6

Query Match 85.8%; Score 2553; DB 4; Length 568;
Best Local Similarity 84.1%; Pred. No. 3e-238;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAPFPEYLEIEVYSTKAKNYNGHCTKTEPQOLAMSVVTLTVMGYEFV 60
DB 1 MPSTDLMLKDFPEYLEIEVYSTKAKNYNGCTKTEPQOLAMSVLTLTVWYELI 60
QY 61 FQESLSMRKKKCFKLTTRKMPIIGRKIODLKNKTDDISKNSFLKVDKEYKALPSOG 120
DB 61 FQESLSMRKKKFLFKIRKMPFIRGRIEQVSKAKKDLVKNMPLKVDYKTLPAOG 120
QY 121 LSSAVLEKIKETSSMDAFQEGRASGVYSGEKKLTLLVYKAYGDPFAMNPLHPIFP 180
DB 121 MGTAELERLEKESYSDMGQEGKASGAVYNGEPKLTLLVQAYGETWSPNPLHPIFP 180
QY 181 LRKLEIYVMTCSLFGNGDSCGCVTSGSTESILMACRACRDLAFKGIKTEPIVAP 240
DB 181 LRKLEIYVMTCSLFGNGDSCGCVTSGSTESILMACRACRDLAFKGIKTEPIVAP 240
QY 241 AHAFAKKAHYFGMKIVRPLTKMEVDVAMRRATSRNTAMLCSTPQPHGVMDVPE 300
DB 241 AHAFAKKAHYFGMKIVRPLTKMEVDVAMRRATSRNTAMLCSTPQPHGVMDVPE 300
QY 301 VAKLAVKYYKIPLVNDAICLGGFLVFMKAGYPLEHPDFRVKGVTSISADTHKYGAP 360
DB 301 VAKLAVKYYKIPLVNDAICLGGFLVFMKAGYPLEHPDFRVKGVTSISADTHKYGAP 360
QY 361 SSVLVSDKKRYNOFFVDMDGGIYASPTISGSPRGISACMAALMHFGNGYEAT 420
DB 361 SSVLVSDKKRYNOFFVDMDGGIYASPTISGSPRGISACMAALMHFGNGYEAT 420
QY 421 KQIKTARFLKSELENIKIFVGNPOLSLIALGSDFDIYRLSNLTAKGWLNOLOFP 480
DB 421 KQIKTARFLKSELENIKIFVGNPOLSLIALGSDFDIYRLSNLTAKGWLNOLOFP 480
QY 481 PSIHFCITLLHAKRVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNVAE 540
DB 481 PSIHFCITLLHAKRVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNVAE 540
QY 541 LSSVFLDSLYSTDTVTOGSONGSPKP 567
DB 541 LSSVFLDSLYSTDTVTOGSONGSPKP 567

RESULT 9
US-08-939-309-10
; Sequence 10, Application US/08939309
; Patent No. 6423527
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Maki J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-939-309-10

Query Match 83.9%; Score 2498; DB 4; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

1 MPSTDLMLKAEPEYLEIEVYSTAKNVNCHCTKYEPMOLIANSVWTLIIWGYEFV 60
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61 POPESIMSRFKKCKRTRKMPILIGRKIDDKLTKDLSKMSFLKVDKEYKALPSSG 120
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241 AHAANAKASYFGMKIVRPPLTKMMEVDVRAARRAISRTAMLVCSSTQFPFGVIDPYE 300
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301 VAKLAVKKYKIPLHVACLGGLIIVEMERAGYPLEHPDFRVKGVTSISADTHK 360
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421 KOIITARFLKSELENIGKIFVFGNPOSLIALGSRDPDIYPLSNLMTAKGNLQLOFP 480
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364 -----LENIGKIFVFGNPOSLIALGSRDPDIYPLSNLMTAKGNLQLOFP 400
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401 PSIHFCITLLHARKKVAIQFLKDIESVTOIKMKNPKAKTTGALYAAOQTVDRNVAE 460
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541 LSSVFLDSLSTDTVTQSGQNMGSPKPH 568
461 LSSVFLDSLSTDTVTQSGQNMGSPKPH 488

RESULT 10
US-09-849-180-10
Sequence 10, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-849-180-10

Query Match 83.9%; Score 2498; DB 4; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

1 MPSTDLMLKAEPEYLEIEVYSTAKNVNCHCTKYEPMOLIANSVWTLIIWGYEFV 60
1 MPSTDLMLKAEPEYLEIEVYSTAKNVNCHCTKYEPMOLIANSVWTLIIWGYEFV 60
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121 LSSSAVLEKLEKSSMDAFWQEGRASGVYSGEEKITELLVAKYAGDFAMSNPLHDPFG 180
121 LSSSAVLEKLEKSSMDAFWQEGRASGVYSGEEKITELLVAKYAGDFAMSNPLHDPFG 180
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181 LKRIAEIVRIACSLFNGGPDSCGCVTSGETSILMACACBDLAFKGIKTPETIAPQS 240
241 AHAANAKASYFGMKIVRPPLTKMMEVDVRAARRAISRTAMLVCSSTQFPFGVIDPYE 300
241 AHAANAKASYFGMKIVRPPLTKMMEVDVRAARRAISRTAMLVCSSTQFPFGVIDPYE 300
301 VAKLAVKKYKIPLHVACLGGLIIVEMERAGYPLEHPDFRVKGVTSISADTHKGYAPKG 360
301 VAKLAVKKYKIPLHVACLGGLIIVEMERAGYPLEHPDFRVKGVTSISADTHK 360
301 VAKLAVKKYKIPLHVACLGGLIIVEMERAGYPLEHPDFRVKGVTSISADTHK 360
361 SSLVLVSDKKYRNYPFVDTMOGGIYASPTIAGSRPGISAAACMAALMHFGENGYEAT 420
361 SSLVLVSDKKYRNYPFVDTMOGGIYASPTIAGSRPGISAAACMAALMHFGENGYEAT 420

Db 354 ----- 353
QY 421 KOIKTARFLKSELENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGNLNOLOFP 480
Db 354 -----LENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGNLNOLOFP 400
QY 481 PSIHFCITLLHAKRRAVIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNMVAE 540
Db 401 PSIHFCITLLHAKRRAVIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNMVAE 460
QY 541 LSSVFLDSLSTDTVTGOSOMNGSPKPH 568
Db 461 LSSVFLDSLSTDTVTGOSOMNGSPKPH 488

RESULT 11

US-09-356-643B-10
; Sequence 10, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-356-643B-10

Query Match 83.9%; Score 2498; DB 4; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MSTDLMLKAPPEYLEIEVYSTKAKNVNGHCTYEPPQOLIANSVWTLTVMGYEFV 60
Db 1 MSTDLMLKAPPEYLEIEVYSTKAKNVNGHCTYEPPQOLIANSVWTLTVMGYEFV 60
QY 61 POPESLMSRFKKCKFLTRKMPITGRKIDKLNTKDDISKNSFLKVDKEYKALPSOG 120
Db 61 POPESLMSRFKKCKFLTRKMPITGRKIDKLNTKDDISKNSFLKVDKEYKALPSOG 120
QY 121 LSSSAVLEKLEKYSMDAFWQEGRASGTYVSGEKLTELLVKAAGDFPANSNPLHPDIFPG 180
Db 121 LSSSAVLEKLEKYSMDAFWQEGRASGTYVSGEKLTELLVKAAGDFPANSNPLHPDIFPG 180
QY 181 LRKIEAEIYRIACSLNENGGPDSCGCVTSSTGESILMACACRDLAEKGIKTEIYAPOS 240
Db 181 LRKIEAEIYRIACSLNENGGPDSCGCVTSSTGESILMACACRDLAEKGIKTEIYAPOS 240
QY 241 AHAFAFKKASYSFGMKIVRPVLTMMEDVYRAMRRASIRNTAMLVCTPOPHGVIPVPE 300
Db 241 AHAFAFKKASYSFGMKIVRPVLTMMEDVYRAMRRASIRNTAMLVCTPOPHGVIPVPE 300
QY 301 VAKLAVKYPILPHVDAACGLIVEMKAGYPLEHPDFRKGVTISADTHKYYAPKG 360
Db 301 VAKLAVKYPILPHVDAACGLIVEMKAGYPLEHPDFRKGVTISADTHKYYAPKG 360
QY 361 SSVLYLSDKKYRYOQFVDTMGQGIYASTINGSPRGGISAACMAALMHFGNGYVEAT 420
Db 361 SSVLYLSDKKYRYOQFVDTMGQGIYASTINGSPRGGISAACMAALMHFGNGYVEAT 420
QY 421 KOIKTARFLKSELENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGNLNOLOFP 480
Db 421 KOIKTARFLKSELENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGNLNOLOFP 480
QY 481 PSIHFCITLLHAKRRAVIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNMVAE 540
Db 481 PSIHFCITLLHAKRRAVIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNMVAE 540

Db 401 PSIHFCITLLHAKRRAVIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTVDRNMVAE 460
QY 541 LSSVFLDSLSTDTVTGOSOMNGSPKPH 568
Db 461 LSSVFLDSLSTDTVTGOSOMNGSPKPH 488

RESULT 12

US-09-356-643B-11
; Sequence 11, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 552
; TYPE: PRP
; ORGANISM: C. elegans
US-09-356-643B-11

Query Match 36.3%; Score 1082; DB 4; Length 552;
Best Local Similarity 42.7%; Pred. No. 6.8e-96;
Matches 228; Conservative 97; Mismatches 197; Indels 12; Gaps 7;

QY 30 VNGHCTYEPPQOLIA-----ANSVWTLTVMGYEFVPOPESLMSRFKKCKFLTRKMPITIG 85
Db 22 INDRLSRYPDVVLVLAFGSTLYTVKYV---HLTKSEDPILRMGAYVSLRKLPAYR 78
QY 86 RKIDKLNTKDDISKNSMFLKVDKEYKALPSOGLSSSAVLEKLEKYSMDAF-WQEGR 144
Db 79 DKIEKLEAKKPKLIESIHDKDKOIFISLPIAPOSIMELAKKEDYNTFNFINIGGR 138
QY 145 ASGTYVSGEE-KTELLVYRAGDFPANSNPLHPDIFPGCLRKIEAEIYRIACSLNENGGPDSC 203
Db 139 VSGAYVYDRAAEHINILGKIYERKAFNSNPLHPDVPFPAARMEMELRLMYLNLNNGPEDSS 198
QY 204 GCVTSSTGESILMACACRDLAEKGIKTEIYAPOSAHAFAFKKASYSFGMKIVRPVLTGR 263
Db 199 GSVTSSTGESITMACSYRRRAHSLGIEHVIILACTAHAFAFKKAAHLGMRRLRHPVDS 258
QY 264 MMEVDYRAMRRASIRNTAMLVCTPOPHGVIPVPEVAKLAVKYPILPHVDAACGLFLT 323
Db 259 DNRVDLKEMRLLDSNVCMVGSAPNPESGTDIPIELAKLGKYGIPVHVDACLGFM 318
QY 324 VPEKAGYPLEHPDFRKGVTISADTHKYYAPKGSSSVLYLSDKKYRYOQFVDTMGQ 383
Db 319 PFMNNDAGY-LIPEFDRNPVTSISCDTHKYYGCTPGSSSVLYMRSKLHMFQFVSADWC 377
QY 384 GGIIYASTINGSPRGGISAACMAALMHFGNGYVEATKOIKTARFLKSELENIKGFV 443
Db 378 GGIIYASTINGSPRGGISAACMAALMHFGNGYVEATKOIKTARFLKSELENIKGFV 437
QY 444 GNPOLSLIALGSRDPDIYRLSNLMTAKGNLNOLOPPSIHFCITLLHAKRRAVIOFLK 503
Db 438 GKSDVSLVAFSGNGVNIYEVSDKMMKLGMLNLTLPNPAIHIICLTINQANAEVVAFAVD 497
QY 504 IRESYVOI-WKNPRAKTTGMAIYAMAQTVDRNMVAELSSVFLDSLSTDTVT 556
Db 498 LEKICELELAKGQKADSGMAAMYGM-AQVPRSVDEVETALYIDATYAPSPST 550

RESULT 13

US-08-939-309-6
; Sequence 6, Application US/08939309
; Patent No. 6423527
; GENERAL INFORMATION:


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Db      304 DACIGGLPFLPEED----EIRYDFRYPGVSSISADSHKYGGLAPKGSVVLYRNKKEHLHN 359
QY      375 QEFVVDWMGGIYASPTIAGSRPGISACALMHGEGYVEATQIITKARFLKSEL 434
Db      360 QYFCDAWMOGGIYASATMEGSRAGHNITACMAALYHAQEGYANAKIYDTYRKIRNGL 419
QY      435 ENIKGIFFVGNPOLSLIALGSRD-FDIYRLSNLMTAKGNLNOLOPPSIHFCTTLHAR 493
Db      420 SNIKGIRKLGPSDVCISWTTNGVELYRPHNEMKEKHQNLNGLOFPAGHIWVTMNH 479
QY      494 KRAVAIOFLKDIRESVTQIM--KNPKAKTGMGAITYAMAQTVDNRNVAELSSVFLDSL 551
Db      480 PGLAEAFVADCRAAVEFVKSHKPSSEDKTSEAAIYGIAQSIIPDRSLVHEFAHSYIDAVYA 539

RESULT 15
US-09-356-643B-4
; Sequence 4, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: C. elegans
US-09-356-643B-4
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Query Match      33.9%; Score 1008; DB 4; Length 542;
Best Local Similarity 38.1%; Pred. No. 9.6e-89;
Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;
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QY      19 LEVYSTAKNYVGHCTKYRPMOLIAVYWTLLIYGYEVPFOPESLMSRFKKCKPKLT 78
Db      5 LEQYHS-AKDLLIFELRKFNPIVLSSTIVATYVLTNLRHMHLEDMGIRKRLSTWFETTV 63
QY      79 RKMPIIGRKIQDKLNTKTKDIDISKNMSFLKYDKYKALPQGLSSAVLEKIKESMDA 138
Db      64 KRVPFIKKMITDKOLNEKDELEKSLRIYDRSTETFTTIPSHVSGRTVEVLRILAIYDDLEG 123
QY      139 -FWQGRASGVYSGEEKL--TELLVYAGDFAMSNLHPDIFPGLRIEAEIYRIACSL 195
Db      124 PAFLEGVSGAVFRNREDDKEREYEVFGKFMNTNIMPKLFPQVARIEMAEVYRMCCNM 183
QY      196 FNGPDSGCVTSGGTESIIMACKACRDIAFEKIGKTPETIYAPQSAHAFAFNKASVFGMK 255
Db      184 MNGDSETCGTMTSGSISILLACLAHNRRLKREKYTEMIIVPSVHAFAEFAECERIK 243
QY      256 IIVVPLTKM-MEVDVYRAMBRAISNMTAMLCSPQRPFGHYIDPPEVAKLAVKKYKTIPLHY 314
Db      244 VRKIPVDPVTFPKVDLVKKAALNKRCMLVGSAPNFPFGTVDDIEALIGQLGLEVDIPVHV 303
QY      315 DACLGFLIVFMERAGYPLHPDFRKYGYTSISADTHKYGAPKGSLLVYSDPKKRYNY 374
Db      304 DACIGGLPFLPEED----EIRYDFRYPGVSSISADSHKYGGLAPKGSVVLYRNKKEHLHN 359
QY      375 QEFVVDWMGGIYASPTIAGSRPGISACALMHGEGYVEATQIITKARFLKSEL 434
Db      360 QYFCDAWMOGGIYASATMEGSRAGHNITACMAALYHAQEGYANAKIYDTYRKIRNGL 419
QY      435 ENIKGIFFVGNPOLSLIALGSRD-FDIYRLSNLMTAKGNLNOLOPPSIHFCTTLHAR 493
Db      420 SNIKGIRKLGPSDVCISWTTNGVELYRPHNEMKEKHQNLNGLOFPAGHIWVTMNH 479
QY      494 KRAVAIOFLKDIRESVTQIM--KNPKAKTGMGAITYAMAQTVDNRNVAELSSVFLDSL 551
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Db      480 PGLAEAFVADCRAAVEFVKSHKPSSEDKTSEAAIYGIAQSIIPDRSLVHEFAHSYIDAVYA 539

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Job time : 28 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 12:36:00 : Search time 50 Seconds
(without alignments)
1803.134 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MPSTDLMLKAFEPYLEIL.....LYSDIVTQSGSOMNGSPKPH 568

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2977	100.0	568	20	AAV05827
2	2959	99.4	568	20	AAV15211
3	2959	99.4	568	22	AAW78461
4	2952	99.2	580	22	AAW79445
5	2553	85.8	568	20	AAV05826
6	2498	83.9	488	20	AAV05830
7	1344	45.1	545	22	ABB64094
8	1344	45.1	545	22	ABB64099
9	1344	45.1	545	22	AAE03543

10	1008	33.9	542	20	AAV05828
11	1007.5	33.8	589	20	AAV05829
12	1007.5	33.8	589	22	AAV07065
13	949	31.9	589	22	AAV07065
14	514.5	17.3	384	22	AAV05828
15	355	11.9	76	20	AAV15211
16	275	9.2	133	21	AAV23455
17	261.5	8.8	466	23	AAV54627
18	258.5	8.7	125	21	AAV23456
19	258.5	8.7	466	23	AAV54627
20	234	7.9	467	23	AAV05828
21	233.5	7.8	496	23	AAV05828
22	233	7.8	500	23	AAV05828
23	232.5	7.8	464	23	AAV05828
24	230.5	7.7	514	22	AAV05828
25	230	7.7	502	23	AAV05828
26	229	7.7	112	22	AAV05828
27	229	7.7	112	22	AAV05828
28	228.5	7.7	496	23	AAV05828
29	227	7.6	502	23	AAV05828
30	226	7.6	494	23	AAV05828
31	226	7.6	494	23	AAV05828
32	225	7.6	101	21	AAV05828
33	218.5	7.3	462	23	AAV05828
34	211.5	7.1	494	23	AAV05828
35	211.5	7.1	494	23	AAV05828
36	209	7.0	502	23	AAV05828
37	207.5	7.0	494	21	AAV05828
38	207.5	7.0	507	21	AAV05828
39	203.5	6.8	464	21	AAV05828
40	202	6.8	500	23	AAV05828
41	202	6.8	500	23	AAV05828
42	198	6.7	493	23	AAV05828
43	198	6.7	493	23	AAV05828
44	181	6.1	609	22	AAV05828
45	180.5	6.1	1042	22	AAV05828

ALIGNMENTS

RESULT 1	AAV05827	standard; Protein: 568 AA.
ID	AAV05827	
AC	AAV05827	
DT	02-AUG-1999	(first entry)
DE	Human sphingosine-1-phosphate lyase.	
KW	Sphingosine-1-phosphate lyase; SPL; human; breast cancer;	
KW	diagnosis; prognosis; therapy.	
OS	Homo sapiens.	
PN	W09916888-A2.	
PD	08-APR-1999.	
PF	29-SEP-1998;	98MO-US20365.
PR	29-SEP-1997;	97US-0933309.
PA	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.	
PI	Saba JD, Zhou J;	
DR	WPT: 1999-263700/22.	
DR	N-PSDB: AAX25567.	
PT	Sphingosine-1-phosphate lyase, polynucleotides and modulators	

C. elegans sphingo
yeast sphingosine-
S cerevisiae apopt
C. albicans apoptos
Putative P. abyssi
Sphingosine-1-phos
Arabidopsis thaliana
Lactococcus lactis
Arabidopsis thaliana
L. lactis M61316 g
Listeria monocytog
Tobacco GAD1. Nic
Petunia GAD protein
Listeria monocytog
A. oryzae glutamate
Herbicidally activ
Lipid degradation
P. patens lipid met
Tobacco GAD2. Nic
A. thaliana GAD1.
A. thaliana GAD2.
Herbicidally activ
Arabidopsis thaliana
Listeria monocytog
A. thaliana GAD5.
Herbicidally activ
Tomato GAD protein
Arabidopsis thaliana
Arabidopsis thaliana
A. thaliana GAD3.
Herbicidally activ
A. thaliana GAD4.
Herbicidally activ
Novel human diagno

PS Claim 9: Page 72-75; 96pp: English.

CC The present sequence represents human endogenous

CC sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the

CC cleavage of sphingosine-1-phosphate into inactive metabolites.

CC Sphingosine-1-phosphate is an endogenous tumour suppressor lipid

CC that potentially inhibits breast cancer cell growth and invasiveness,

CC while not affecting the growth of non-tumour cells. Mouse and

CC human SPL polynucleotides (see AAX25666-67) and polypeptides (see

CC AAY05826-29) are claimed. Methods are provided for preparing SPL

CC using transformed or transfected host cells. SPL polypeptides are

CC used in claimed methods for identifying agents that modulate SPL

CC activity. An SPL inhibitor will inhibit growth of cancer cells,

CC especially breast cancer cells. SPL inhibitors (polynucleotides

CC preventing expression of SPL genes, or antibodies against SPL) can

CC also be used to prevent the development and/or metastasis of

CC cancer, especially where the inhibitor is linked to an antitumour

CC or antileptrogen receptor antibody. Detection of alterations in an

CC endogenous SPL sequence, especially where the alteration is a

CC deletion of residues 354-433 of the 568 amino acid human SPL

CC sequence (see also AAY05830), can be used to diagnose cancer, and to

CC assess the prognosis for recovery.

XX Sequence 568 AA:

Query Match 100.0%; Score 2977; DB 20; Length 568;
Best Local Similarity 100.0%; Pred. No. 1.4e-281;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLVWGEYEV 60
DB 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLVWGEYEV 60
QY 61 FQESLMSRFKKCKFLTRKMPITGRKIDKLKTKDIDSKNMSFLKVDKEYKALPSSG 120
DB 61 FQESLMSRFKKCKFLTRKMPITGRKIDKLKTKDIDSKNMSFLKVDKEYKALPSSG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
QY 181 LKRIEAEIYRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
DB 181 LKRIEAEIYRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
QY 241 AHAFAFKKASYSFGMKIVRVPPLTKMEVDVRAHRAISRNTAMLYCSTPQPPHGVDPVE 300
DB 241 AHAFAFKKASYSFGMKIVRVPPLTKMEVDVRAHRAISRNTAMLYCSTPQPPHGVDPVE 300
QY 301 VAKLAVKXKIPHLVDACLGFLVFEKAGYPLEHPDFRVKGVTSISADTRKYGYPKG 360
DB 301 VAKLAVKXKIPHLVDACLGFLVFEKAGYPLEHPDFRVKGVTSISADTRKYGYPKG 360
QY 361 SSVLYVSDKKRYRNOFEVDTDGOGIYASPTIAGSRPGGISAACMAALHFGNGVEAT 420
DB 361 SSVLYVSDKKRYRNOFEVDTDGOGIYASPTIAGSRPGGISAACMAALHFGNGVEAT 420
QY 421 KOIKTARFLKSELEIKIFVEGNPOLSLIALGSDPDIYRLSNLMTAKGNLNDLOPP 480
DB 421 KOIKTARFLKSELEIKIFVEGNPOLSLIALGSDPDIYRLSNLMTAKGNLNDLOPP 480
QY 481 PSIHFCITLLHAKRVAIOFLKDIRESVTQIMKNPRAKTTGMAIYAMAQTVDRMVAE 540
DB 481 PSIHFCITLLHAKRVAIOFLKDIRESVTQIMKNPRAKTTGMAIYAMAQTVDRMVAE 540
QY 541 LSSVFLDSLXSTDTVYQSGOMNGSPKPH 568
DB 541 LSSVFLDSLXSTDTVYQSGOMNGSPKPH 568

RESULT 2
AAY15211
ID AAY15211 standard; Protein; 568 AA.

XX AAY15211;
AC 26-OCT-1999 (first entry)
DT Sphingosine-1-phosphate lyase amino acid sequence.
XX
DE Sphingosine-1-phosphate; sphingosine-1-phosphate lyase; SPHINGLY;
KW G-protein coupled receptor; EDG-1; secondary messenger; cancer;
KW cardiovascular disorder; thrombosis; atherosclerosis; wound healing;
KM stroke; apoptosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..568
ET /label= "Sphingosine-1-phosphate lyase"

XX WO9938983-A1.
XX 05-AUG-1999.
XX
XX 24-DEC-1998; 98WO-EP08564.
XX
XX 03-NOV-1998; 98GB-0024026.
XX 29-JAN-1998; 98EP-0300625.
XX
XX (SMK) SMITHKLINE BEECHAM PLC.

PI Duckworth DM, Godden RJ, Testa TR;
XX WPI; 1999-479192/40.
XX
XX N-PSDB; AAZ06342.

PT A new sphingosine-1-phosphate lyase useful for diagnosing and
PT treating cancers, cardiovascular disorders, thrombosis or
PT atherosclerosis

XX Claim 1; Page 23-24; 37pp: English.

CC This is the amino acid sequence of Sphingosine-1-phosphate lyase. The
CC lyase catalyses the cleavage of Sphingosine-1-phosphate to give a long
CC chain aldehyde and phosphoethanolamine.
CC The sequence has use as a method of treating cancers, cardiovascular
CC disorders, thrombosis, atherosclerosis and other conditions. This is due
CC to the action of Sphingosine-1-phosphate intracellularly as a secondary
CC messenger and extracellularly as a ligand for the G-protein coupled
CC receptor EDG-1.

XX Sequence 568 AA:

Query Match 99.4%; Score 2959; DB 20; Length 568;
Best Local Similarity 99.5%; Pred. No. 7.9e-280;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLVWGEYEV 60
DB 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLVWGEYEV 60
QY 61 FQESLMSRFKKCKFLTRKMPITGRKIDKLKTKDIDSKNMSFLKVDKEYKALPSSG 120
DB 61 FQESLMSRFKKCKFLTRKMPITGRKIDKLKTKDIDSKNMSFLKVDKEYKALPSSG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
QY 181 LKRIEAEIYRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
DB 181 LKRIEAEIYRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
QY 241 AHAFAFKKASYSFGMKIVRVPPLTKMEVDVRAHRAISRNTAMLYCSTPQPPHGVDPVE 300
DB 241 AHAFAFKKASYSFGMKIVRVPPLTKMEVDVRAHRAISRNTAMLYCSTPQPPHGVDPVE 300

Db 2A1 AHAFAFNKASVFGMKIVRPLTKMMEVDVRAARRAISRNTAMLCSTPQFPFGVIDPVE 300
 QY 301 VAKLAVKKYKIPLVHACLGGLIIVMEKAGYLEHPDFRVRGVTISADTHKYGAPRG 360
 Db 301 VAKLAVKKYKIPLVHACLGGLIIVMEKAGYLEHPDFRVRGVTISADTHKYGAPRG 360
 QY 361 SSVLVSDKKRYNYQFVDTDMOGGIVASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 Db 361 SSVLVSDKKRYNYQFVDTDMOGGIVASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 QY 421 KQIITARFLKSELENIGKIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
 Db 421 KQIITARFLKSELENIGKIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
 QY 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 Db 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
 Db 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 3

AAM78461 ID AAM78461 standard; Protein; 568 AA.
 AC AAM78461;
 DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 1123.
 KM Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US04098.
 PF 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 PA (HYSEQ) HYSEQ INC.
 PI Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK51594.
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 PS Claim 20; Page 3353-3354; 6221pp; English.
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAK80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX SQ Sequence 568 AA:

Query Match 99.4%; Score 2959; DB 22; Length 568;

Best Local Similarity 99.5%; Pred. No. 7.9e-280;

Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKRYEPMOLIAVSVWTLTIWGYEFV 60
 Db 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKRYEPMOLIAVSVWTLTIWGYEFV 60
 QY 61 FQPESLMSRKKKCKRLTKRMPILIGRKIQDKLNTKTDISTKMSFLKVDKEYKALPSOG 120
 Db 61 FQPESLMSRKKKCKRLTKRMPILIGRKIQDKLNTKTDISTKMSFLKVDKEYKALPSOG 120
 QY 121 LSSSAVLEKLEKYESSMDAFWQEGRASGTYVSGEEKTELILYKAGDFANSLHPDIFPG 180
 Db 121 LSSSAVLEKLEKYESSMDAFWQEGRASGTYVSGEEKTELILYKAGDFANSLHPDIFPG 180
 QY 181 LKRIAEIVRIACSLFNGGPDSCGVTSGTESIIMACKACDIAFEKIKTPEIYAPOS 240
 Db 181 LKRIAEIVRIACSLFNGGPDSCGVTSGTESIIMACKACDIAFEKIKTPEIYAPOS 240
 QY 241 AHAFAFNKASVFGMKIVRPLTKMMEVDVRAARRAISRNTAMLCSTPQFPFGVIDPVE 300
 Db 241 AHAFAFNKASVFGMKIVRPLTKMMEVDVRAARRAISRNTAMLCSTPQFPFGVIDPVE 300
 QY 301 VAKLAVKKYKIPLVHACLGGLIIVMEKAGYLEHPDFRVRGVTISADTHKYGAPRG 360
 Db 301 VAKLAVKKYKIPLVHACLGGLIIVMEKAGYLEHPDFRVRGVTISADTHKYGAPRG 360
 QY 361 SSVLVSDKKRYNYQFVDTDMOGGIVASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 Db 361 SSVLVSDKKRYNYQFVDTDMOGGIVASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 QY 421 KQIITARFLKSELENIGKIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
 Db 421 KQIITARFLKSELENIGKIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLQLOFP 480
 QY 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 Db 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
 Db 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
 Db 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
 RESULT 4
 ID AAM79445
 AC AAM79445;
 DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 3091.
 KM Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
XX
PN W0200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001: 2001MO-US04098.
XX
XX 03-FEB-2000: 2000US-0496914.
PR 27-APR-2000: 2000US-0560875.
PR 20-JUN-2000: 2000US-0598075.
PR 19-JUL-2000: 2000US-0620325.
PR 01-SEP-2000: 2000US-0654936.
PR 15-SEP-2000: 2000US-0663561.
PR 20-OCT-2000: 2000US-0693325.
PR 30-NOV-2000: 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PsDB; AAK52578.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20: Page 249: 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW8323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibn activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAW80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX
SQ Sequence 580 AA:
Query Match 99.2%; Score 2952; DB 22: Length 580;
Best Local Similarity 99.3%; Pred. No. 3.9e-279;
Matches 364; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPTDLMKAPEPYLEIEVYSTKAKNVNGHCTKYEPQOLJAMSVMVTLILVWGVEFY 60
DB 13 MPTDLMKAPEPYLEIEVYSTKAKNVNGHCTKYEPQOLJAMSVMVTLILVWGVEFY 72
QY 61 FQESLMSRRKKCKFKLTKRMPIIGRKIDKLKTRKDISKNSFLKVDKEYKALPSOG 120
DB 73 FQESLMSRRKKCKFKLTKRMPIIGRKIDKLKTRKDISKNSFLKVDKEYKALPSOG 132
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGYTSGEEKTELLVKAYGDFANSNPLHPDIFPG 180
DB 133 LSSSAVLEKLEKSSMDAFWQEGRASGYTSGEEKTELLVKAYGDFANSNPLHPDIFPG 192
QY 181 LKRIEAIYRIACSLFNGSGPDSGCVTSGETESIILAKACRDLAPEGKIKTPEIYAPOS 240
DB 193 LKRIEAIYRIACSLFNGSGPDSGCVTSGETESIILAKACRDLAPEGKIKTPEIYAPOS 252
QY 241 AAAAFKKAASYFGMKIVRVPFLTKMMEVDVRAAMRAISRNTAMLCVSTPDPHGVIDPVE 300
DB 253 AAAAFKKAASYFGMKIVRVPFLTKMMEVDVRAAMRAISRNTAMLCVSTPDPHGVIDPVE 312
QY 301 VAKLAVKYLPIHLVDACLGGLIVFMKAGYPLEHFPDRVKGVTISADTHKYGTAAPKG 360

DB 313 VARLAVKYLPIHLVDACLGGLIVFMKAGYPLEHFPDRVKGVTISADTHKYGTAAPKG 372
QY 361 SSLVYSDDKRYRNQFVDFDMOGGIIYASPTIAGSRPGGISAACMAALMHFGENGYEAT 420
DB 373 SSLVYSDDKRYRNQFVDFDMOGGIIYASPTIAGSRPGGISAACMAALMHFGENGYEAT 432
QY 421 KQIIKTARFLKSELENIKGIFVFGNPQLSLIALGSRDFDIYRLSNLMTAKGWLNLQFP 480
DB 433 KQIIKTARFLKSELENIKGIFVFGNPQLSVIALGSRDFDIYRLSNLMTAKGWLNLQFP 492
QY 481 PSTHECTTLHARRRAVIOFLKDIRESVQIMKNPKKTTGMAIYMAQTVDNRNVAE 540
DB 493 PSTHECTTLHARRRAVIOFLKDIRESVQIMKNPKKTTGMAIYMAQTVDNRNVAE 552
QY 541 LSSVFLDSLXTDVTYTGSGMNSPKPH 568
DB 553 LSSVFLDSLXTDVTYTGSGMNSPKPH 580
RESULT 5
ID AAY05826
XX AAY05826 standard; Protein; 568 AA.
XX
XX AAY05826;
XX
XX 02-AUG-1999 (first entry)
XX
XX Mouse sphingosine-1-phosphate lyase.
XX
XX Sphingosine-1-phosphate lyase; SPL; mouse; breast cancer;
KW diagnosis; prognosis; therapy.
XX
XX Mus musculus.
XX
XX W09916888-A2.
XX
XX 08-APR-1999.
XX
XX 29-SEP-1998; 98WO-0620365.
XX
XX 29-SEP-1997; 97US-0939309.
XX
XX (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
XX
XX Saba JD, Zhou J;
XX
XX WPI: 1999-263700/22.
XX
XX N-PsDB; AAX25566.
XX
XX Sphingosine-1-phosphate lyase, polynucleotides and modulators
PS Claim 9: Page 64-67; 96pp; English.
XX
XX The present sequence represents murine endogenous
CC sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the
CC cleavage of sphingosine-1-phosphate into inactive metabolites.
CC Sphingosine-1-phosphate is an endogenous tumour suppressor lipid
CC that potentially inhibits breast cancer cell growth and invasiveness,
CC while not affecting the growth of non-tumour cells. Mouse and
CC human SPL polynucleotides (see AAX25566-67) and polypeptides (see
CC AAY05826-29) are claimed. Methods are provided for preparing SPL
CC using transformed or transfected host cells. SPL polypeptides
CC used in claimed methods for identifying agents that modulate SPL
CC activity. An SPL inhibitor will inhibit growth of cancer cells,
CC especially breast cancer cells. SPL inhibitors (polynucleotides
CC preventing expression of SPL genes, or antibodies against SPL) can
CC also be used to prevent the development and/or metastasis of
CC cancer, especially where the inhibitor is linked to an antitumour
CC or antioestrogen receptor antibody. Detection of alterations in an
CC endogenous SPL sequence can be used to diagnose cancer, and to
XX assess the prognosis for recovery.

SQ Sequence 568 AA:
Query Match 85.8%; Score 2553; DB 20; Length 568;
Best Local Similarity 84.1%; Pred. No. 3.8e-240;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEPYLEILEYVSTKAKNVVGHCTKYPQOLIAMSVVMTLLIYWGEFV 60
DB 1 MPSTDLMLKAFEPYLEILEYVSTKAKNVVGHCTKYPQOLIAMSVVMTLLIYWGEFV 60
QY 61 FQPSLMSRFKKKCFKLTRKMPITGRKIQDLNKTDDISNMSEFLKDYKAYALPSQG 120
DB 61 FQPSLMSRFKKKCFKLTRKMPITGRKIQDLNKTDDISNMSEFLKDYKAYALPSQG 120
QY 121 LSSAVLEKLEKESMDAFMOGRASGVTVSGEEKLTBLKAYGDFAMSNPLHDPDPG 180
DB 121 MGTAEVLERLEKESMDAFMOGRASGVTVSGEEKLTBLKAYGDFAMSNPLHDPDPG 180
QY 181 LRKIEAEIVRIACSLFNGGPDSCGCVTSGTSTILMACACRDALFEKIGITPEIVAPQS 240
DB 181 LRKIEAEIVRIACSLFNGGPDSCGCVTSGTSTILMACACRDALFEKIGITPEIVAPQS 240
QY 241 AHAAFNKAASYFGMKIYRVPLTKMEVDVYRAMRRAISNTAMLCSTPQFPHGYIDPVE 300
DB 241 AHAAFNKAASYFGMKIYRVPLTKMEVDVYRAMRRAISNTAMLCSTPQFPHGYIDPVE 300
QY 301 VAKLAVKXKIPDLHVDACLGFLIVFMEKAGYPLEHPDFRKYGVTSISADTHKGYAPKG 360
DB 301 VAKLAVKXKIPDLHVDACLGFLIVFMEKAGYPLEHPDFRKYGVTSISADTHKGYAPKG 360
QY 361 SSLVLYSDKKYRNQFVDTDMOGGIVASPTIAGSRPGISACMAALMHFGNGYVEAT 420
DB 361 SSLVLYSDKKYRNQFVDTDMOGGIVASPTIAGSRPGISACMAALMHFGNGYVEAT 420
QY 421 KOIITARFLKSELENKIGIFVFGNPOLSLIALSRDPIRLSNLMTAKGMNLQLOFP 480
DB 421 KOIITARFLKSELENKIGIFVFGNPOLSLIALSRDPIRLSNLMTAKGMNLQLOFP 480
QY 481 PSIHFCITLLHARRKVAIOFLKDIRESYTOIMKNPKAKTTGMAIYMAOQTVDNRNVAE 540
DB 481 PSIHFCITLLHARRKVAIOFLKDIRESYTOIMKNPKAKTTGMAIYMAOQTVDNRNVAE 540
QY 541 LSSVFLDSLSTDTVTQSGOMNGSPKP 567
DB 541 LSSVFLDSLSTDTVTQSGOMNGSPKP 567

RESULT 6
AA05830
ID AA05830 standard; Protein: 488 AA.
AC AA05830;
XX 02-AUG-1999 (first entry)
XX Human altered sphingosine-1-phosphate lyase.
DE Sphingosine-1-phosphate lyase; SPL; human; breast cancer;
KW diagnosis; prognosis; therapy; deletion.
XX Homo sapiens.
OS
XX
XX MO9916888-A2.
XX
XX 08-APR-1999.
XX
XX 29-SEP-1998; 98WD-US20365.
XX
XX 29-SEP-1997; 97US-0939309.
XX
XX (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
XX
XX Saba JD, Zhou J;
PI

XX WP1: 1999-263700/22.
DR N-PSDB; AAX25570.
XX Sphingosine-1-phosphate lyase, polynucleotides and modulators
PI Example 3; Page 94-96; 96pp; English.

XX The present sequence represents sphingosine-1-phosphate lyase (SPL),
CC as predicted from cDNA (see AAX25570) obtained by amplification of
CC human glioblastoma multiforme RNA. The polypeptide sequence lacks
CC amino acids 354-433 of SPL (see AAY05827) predicted from a clone
CC obtained from fibroblast cells. Sphingosine-1-phosphate is an
CC endogenous tumour suppressor lipid that potentially inhibits breast
CC cancer cell growth and invasiveness, while not affecting the growth
CC of non-tumour cells. Detection of alterations in an endogenous SPL
CC sequence, especially where the alteration is a deletion of residues
CC 354-433 of the 568 amino acid human SPL sequence, can be used to
CC diagnose cancer, and to assess the prognosis for recovery. Mouse and
CC human SPL polynucleotides (see AAX25666-67) and polypeptides (see
CC AAY05826-29) are claimed. The polypeptides are used in claimed methods
CC for identifying agents that modulate SPL activity. SPL inhibitors
CC will inhibit growth of cancer cells, especially breast cancer cells.
CC They can also be used to prevent the development and/or metastasis
CC of cancer, especially where the inhibitor is linked to an anti-tumour
CC or anti-oestrogen receptor antibody.

SQ Sequence 488 AA:
Query Match 83.9%; Score 2498; DB 20; Length 488;
Best Local Similarity 85.9%; Pred. No. 7.1e-235;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MPSTDLMLKAFEPYLEILEYVSTKAKNVVGHCTKYPQOLIAMSVVMTLLIYWGEFV 60
DB 1 MPSTDLMLKAFEPYLEILEYVSTKAKNVVGHCTKYPQOLIAMSVVMTLLIYWGEFV 60
QY 61 FQPSLMSRFKKKCFKLTRKMPITGRKIQDLNKTDDISNMSEFLKDYKAYALPSQG 120
DB 61 FQPSLMSRFKKKCFKLTRKMPITGRKIQDLNKTDDISNMSEFLKDYKAYALPSQG 120
QY 121 LSSAVLEKLEKESMDAFMOGRASGVTVSGEEKLTBLKAYGDFAMSNPLHDPDPG 180
DB 121 LSSAVLEKLEKESMDAFMOGRASGVTVSGEEKLTBLKAYGDFAMSNPLHDPDPG 180
QY 181 LRKIEAEIVRIACSLFNGGPDSCGCVTSGTSTILMACACRDALFEKIGITPEIVAPQS 240
DB 181 LRKIEAEIVRIACSLFNGGPDSCGCVTSGTSTILMACACRDALFEKIGITPEIVAPQS 240
QY 241 AHAAFNKAASYFGMKIYRVPLTKMEVDVYRAMRRAISNTAMLCSTPQFPHGYIDPVE 300
DB 241 AHAAFNKAASYFGMKIYRVPLTKMEVDVYRAMRRAISNTAMLCSTPQFPHGYIDPVE 300
QY 301 VAKLAVKXKIPDLHVDACLGFLIVFMEKAGYPLEHPDFRKYGVTSISADTHKGYAPKG 360
DB 301 VAKLAVKXKIPDLHVDACLGFLIVFMEKAGYPLEHPDFRKYGVTSISADTHKGYAPKG 360
QY 361 SSLVLYSDKKYRNQFVDTDMOGGIVASPTIAGSRPGISACMAALMHFGNGYVEAT 420
DB 361 SSLVLYSDKKYRNQFVDTDMOGGIVASPTIAGSRPGISACMAALMHFGNGYVEAT 420
QY 421 KOIITARFLKSELENKIGIFVFGNPOLSLIALSRDPIRLSNLMTAKGMNLQLOFP 480
DB 421 KOIITARFLKSELENKIGIFVFGNPOLSLIALSRDPIRLSNLMTAKGMNLQLOFP 480
QY 481 PSIHFCITLLHARRKVAIOFLKDIRESYTOIMKNPKAKTTGMAIYMAOQTVDNRNVAE 540
DB 481 PSIHFCITLLHARRKVAIOFLKDIRESYTOIMKNPKAKTTGMAIYMAOQTVDNRNVAE 540
QY 541 LSSVFLDSLSTDTVTQSGOMNGSPKP 568
DB 541 LSSVFLDSLSTDTVTQSGOMNGSPKP 568

RESULT 7
ABB64094
ID ABB64094 standard; Protein; 545 AA.
XX AC ABB64094;
XX XX
DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 19074.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
PE 23-MAR-2001; 2001WO-US09231.
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-061415O.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
DR N-PsDB; ABL08197.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Disclosure; SEQ ID NO 19074; 21pp + Sequence Listing; English.
PS xx
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABLI6176-ABLJ3051), expressed DNA
CC sequences (ABLI01840-ABLI6175) and the encoded proteins
CC (AAB57737-ABR72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX CC
XX SQ Sequence 545 AA;
Query Match 45.1%; Score 1344; DB 22; Length 545;
Best Local Similarity 49.0%; Pred. No. 5,5e-122;
Matches 254; Conservative 100; Mismatches 160; Indels 4; Gaps 4.
OY 38 EPMOLIAISVWTLTIIVGGEFEPQESLSMRFKKCKPLPKMKIIGRTKIDKLNTKRD 97
: : : : : : : : : : : : : : :
Dd 25 EPMOVATITATTVGLGVALMTVICODEMLYIRGKRQFKFRAKTIAVRROYETELAAKN 84
: :
OY 98 DISKMMSFLVKDEYKVALPSOGSSSAVLEKTKYESMDAF-WQGRASGTVYSGEERL 156
: :
Dd 85 DFETFIKSNHLTFSTLPKGLSKEILRLVDHCLKTGHNMRDGRVSGAVGYKPDLL 144
: :
OY 157 TELLVKAGCDRAWSRPHLDIFPGLRKTLEAEIVRACSLFNNGGPSCGCVISGGESTILM 216
: :
Dd 145 VELTEVYGKASYTNPLHADLFPGCKMEAEVVRMACNLFHGNSASCGETMTGTGESITYM 204
: :
OY 217 ACKACRDIAFE-KGIGTPEIVAPOSANAHAFNKASYPFCMKTVIRVPL-TKRMEDVBRAMR 274
: : : : : : : : : : : : : : : : :
Dd 205 AMKAVIRDPAREKETGITRNINIVPEKTYVHAFLDKGGCYFINIHRSVDVDEPTYEVDIKRRR 264
: :
OY 275 AISRNTAMLVCSTPQFPGHVIDPVPEVAKLAVKKRIPLHDVADCLGELLIVEMERAGPYLE 334

Db	265	AIKNTITLLGSGAPNPEPTITDIDEIAIALGKVIDIPVHVDCCSFVVALVRNAGKYL	322
QY	335	HPPEFVKYGTSTISADTHKXGAPKSSVLVLSDRKRYNOFEYDMDGGIVASPTIAG	394
Db	324	RPDFEYKGVTSISADTHKXGAPKSSVLVLSDRKRYNOFEYDMDGGIVASPTIAG	383
QY	395	SRPGSIGAACMAALHMGENGIVEATKQIITKARFLKSELENIKCIFVGNPQLSLALG	454
Db	384	SRAGGIIIAACMAATMSEFGDYLEAKRKRIVDARVIERGVRIQIGIFFGKPAVSIALG	443
QY	455	SRDDIDIRLSNLTAKGWNLNOLQPPPSIHFCITITLLHARKRYAIOFLKIDRESVTOIMKN	514
Db	444	SNVFDIRLSDSCJCKGMNLSALQEPSSGTHLCVTDMHTQPGVADKFLADVRSCTAETMKD	503
QY	515	PKAKTTGMAIVAAQTVDVNNVVELSSVFLDSLSTY 552	
Db	504	PGCPYVGKMAALYGMASIPDRSVIGEVTRLFLHSHWYT 541	
RESULT 8			
ABB64099			
ID	ABB64099	standard; Protein; 545 AA.	
AC	ABB64099;		
DT	26-MAR-2002	(first entry)	
DE	Drosophila melanogaster	polypeptide SEQ ID NO 19089.	
XX	Drosophila	developmental biology; cell signalling; insecticide;	
KM	pharmaceutical.		
XX	Drosophila melanogaster.		
OS	WO200171042-A2.		
PN	27-SEP-2001.		
XX	23-MAR-2001;	2001WO-US09231.	
PF	23-MAR-2000;	2000US-191637P.	
PR	11-JUL-2000;	2000US-0614150.	
XX	(PEKE)	PE CORP NY.	
PA	Venter JC, Adams M, Li PWD, Myers EM;		
PI	WPI; 2001-656860/75.		
DR	N-PSDB; ABL08202.		
XX	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
PI	interactions -		
XX	Disclosure; SEQ ID NO 19089; 21pp + Sequence Listing; English.		
PS	The invention relates to an isolated nucleic acid detection reagent		
XX	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (AB161716-AB130511), expressed DNA		
CC	sequences (AB101840-AB161715) and the encoded proteins		
CC	(ABB57737-ABB72072).		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published.pct_sequences.		
XX	Sequence	545 AA;	
QY	Query Match	45.18; Score 1344; DB 22; Length 545;	
XX	Best Local Similarity	49.0%; Pzed No. 5,5e-122;	

[illegible]

Query Match	45.1%	Score 1344	DB 22	Length 545
Best Local Similarity	49.0%	Pred. No. 5,5e-122		
Matches 254	Conservative 100	Mismatches 160	Indels 4	Gaps 4
38	EPWOLIAVWVTLTIWVGEFVDPESILMSFKKKCKLTKRMKIIIRKTIODKLNKRD	97		
Db	25 EPMOYATITATTVVLGVWMLWTVICODENLYIRGKQFRPAKPIAVRQVETELAKKN	84		
QY	98 DISKNMSELVKDYKEVYKALPSQGLSSSAVLEKLEKESMDAF-WQGRASGTVYSGEERL	156		
Db	85 DEETFIKRSNMHLTSETLTPKESKKEITRLVDHLELKTGHYMRDGRVSGAVYGYKPD	144		
QY	157 TELVYKATGDRAMSPLRPDIFFPGRLKEAEIVRACSLFNGPSCCCVYSGESTILM	216		
Db	145 VELTEVYGGKASTNPLHADLEPGVCKKAEAEVVRACNLPHGNSASCCTMTTGTESTIWM	204		
QY	217 ACKACRDIAFE-KGIGTPEIIVAPOSAHNAFNKAASYEFCKIYRVPL-TRKMEVDVRAHR	274		
Db	205 AMKATVRDAREYKGTTRNIYVPRKVHNAFDPKGGYFNHRSVYDDETEYVDLKKRKR	264		
QY	275 AISRNTAMVLCSTPQFPHGVDPVPEVAKLVAKYIKPLHVDACLGELTIVEMKAGYPLE	334		
Db	265 AINRNTILLVTSAPFPGYTDIDDEAIIALGVKKYDIPVHVDACLSGSFVAALVRNAGYKL	323		
QY	335 HPDPDRVGVYSISADTHKYGYPARGSSVLVYSOKKYNNYOFVVDVDMOGIYASPTIAG	394		
Db	324 RPFDEYVGVYSISADTHKYGYPARGSSVLVYSOKKYNDHOFTVYDDMPGGVYSGSPYVNG	383		
QY	395 SRPGISASAAALHFEENGVEYVATKQIIKTARLKSELENKIGTIFFGNPOLSLIALG	454		
Db	384 SRAGIIIAACVATMMSFGYDGLTEATKRIYDARIERGVDRIDGIFIFGRPATSVIALG	443		
QY	455 SRDGDIVLNLMLAKGNNLQLOFPSPYIHNCITILHAKRKVALOFLDIDIESYQIMKN	514		
Db	444 SNVDFIPLDLSLCKLGNLNLALDPSSGIIHLGVDMHOPGVADEIADVRSCTAEIMKD	503		
QY	515 PRAKTTGCAIYAMAQTVTDNRNMAELSVFLDSLSTY 552			
Db	504 PGQPVYCKMAYLGYMAQSTDPSSVGEVYRFLFLSHSYVT 541			

ID	AAI05828	standard; Protein; 542 AA.
XX	AAI05828;	
XX	02-AUG-1999	(first entry)
XX	C. elegans sphingosine-1-phosphate lyase.	
XX	Sphingosine-1-phosphate lyase; SPL; breast cancer; diagnosis;	
XX	prognosis; therapy.	
XX	Caenorhabditis elegans.	
XX	MO9916888-A2.	
XX	08-APR-1999.	
XX	29-SEP-1998;	98MO-US20365.
XX	29-SEP-1997;	97US-0939309.
XX	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.	
XX	Saba JD, Zhou J;	
XX	WPI: 1999-263700/22.	
XX	N-PSDB; AAX25568.	
XX	Sphingosine-1-phosphate lyase, polynucleotides and modulators	
XX	Claim 11; Page 79-82; 96pp; English.	
XX	The present sequence represents Caenorhabditis elegans endogenous	
XX	sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the	
XX	cleavage of sphingosine-1-phosphate into inactive metabolites. Human	
XX	sphingosine-1-phosphate is an endogenous tumour suppressor lipid	
XX	that potentially inhibits breast cancer cell growth and invasiveness,	
XX	while not affecting the growth of non-tumour cells. C. elegans SPL	
XX	is used in a claimed method for identifying agents that modulate	
XX	SPL activity. SPL inhibitors will inhibit growth of cancer cells,	
XX	especially breast cancer cells. SPL inhibitors, including	
XX	polynucleotides preventing expression of SPL genes, or antibodies	
XX	against SPL, can also be used to prevent the development and/or	
XX	metastasis of cancer, especially where the inhibitor is linked to an	
XX	antitumour or antioestrogen receptor antibody. Detection of	
XX	alterations in an endogenous SPL sequence can be used to diagnose	
XX	cancer, and to assess the prognosis for recovery.	
XX	Sequence 542 AA;	
XX	Query Match 33.9%; Score 1008; DB 20; Length 542;	
XX	Best Local Similarity 38.1%; Pred. No. 3.9e-89;	
XX	Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7	
QY	19 LEVSTAKANNVNGCHTVEPMQLIAMSVWTLTIWGYEFYQFESLMSRFFKKCFKLT 78	
DB	5 LEQVYS-AKDLIELFRKFNPIVAVSSIVATVYLTNLRHMLDMDGIRKRLSTWFFETTV 63	
QY	79 RKMPILGKIDDKINKTKDDISKMSFLKVDKEYKALPSQGLSSAVLEKLEKVSMDA 138	
DB	64 KRVPIFRKMDIKQLEWVDELEKSLRIYDRKSTETFTTIPSHSVGRTVELRLAATYDDLEG 123	
QY	139 -FWOGRASGTIVYSESEKLT--TELIVKAYGDFWANSNPILPPIRLKITEAIVIAIACL 195	
DB	124 PAFLEGKRVSGAVFNEEDDKDREMYEEVFGFAWNPILMPKLPFGVRLMEAEVVMCCNM 183	
QY	136 FNGCPDSCGCYVSGCTESILMACAKRDLAEFGKIGTPEIYAPQSAHAFAFNKASTYFGMK 255	
DB	184 MNGSEETGCTSTGSSILLACLAHNRLLKRGKYEYEMIVPSSVHAFAFKAACFPFK 243	

QY	256	YVRVLETKM-MENVDRAMRAISRNTAMLCVSPPOPHGVIDVPEVAKLAVKXKIPLHV	314
Db	244	VAKTIVDPTEFVLDVLYKMAALINKRCMLYGSAPNPFPGVVDIEALIGGLEXPDPVHV	303
QY	315	DACLGGLFLVFMKAGYPLHEPFDFVKCVSTISADTHKYGAPKSSLVLYSDKKYRNY	374
Db	304	DACLGGLFLPFLEED---EIRDFRVPVSSISADSHKXGLAPKSSVLYRNKLELHN	359
QY	375	QEFVVTDMOGGIYASPTINGSRPGGISAAACMAALHFGENGVEATKOITKTARFLKSEL	434
Db	360	QYFCADADMOGGIYASATMGSRAGHNIALCMAAMLHADEGYKANARKIYDTRKIRNGL	419
QY	435	ENIKGIFPVGNGQLSLADGSRD-FDITRLSNIMTKKGNLNLOJOPPSIHFCITLLHAR	493
Db	420	SNIKKIKIKLQGPEDVCIVSTTTDGVLYLFFHNFMRKKHHQLNLOJFPAGVHIMVTNNHTH	479
QY	494	KRAVLOFLKIDIRESVTQIM-KNPKAKTTGMAIYAMAQTVDRNNVAELSSVELDSLVS	551
Db	480	PGLAAFAFVADCRAAVEFVKSHKRPSESDKTSSEAALYGLAQSIDPRSLVHEFAHSYIDAVYA	539
RESULT 11			
AAV05829	AAV05829 standard; protein; 589 AA.		
XX	AAV05829;		
AC			
XX	02-AUG-1999	(first entry)	
DT			
XX			
XX			
DE	Yeast sphingosine-1-phosphate lyase.		
XX			
KW	Sphingosine-1-phosphate lyase; SPL, breast cancer; diagnosis;		
MM	prognosis; therapy; yeast.		
XX			
OS	Saccharomyces cerevisiae.		
XX			
PN	W09916888-A2.		
XX			
PD	08-APR-1999.		
XX			
PF	29-SEP-1998; 98WO-US20365.		
XX			
PR	29-SEP-1997; 97US-0939309.		
XX			
PA	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.		
XX			
PI	Saba JD, Zhou J;		
XX			
PI	WPI; 1999-263700/22.		
XX			
DR	N-PSDB; AAX25569.		
XX			
PT	Sphingosine-1-phosphate lyase, polynucleotides and modulators		
XX			
PS	Claim 11; Page 87-90; 96pp; English.		
XX			
CC	The present sequence represents Saccharomyces cerevisiae endogenous		
CC	sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the		
CC	cleavage of sphingosine-1-phosphate into inactive metabolites. Human		
CC	sphingosine-1-phosphate is an endogenous tumour suppressor lipid		
CC	that potentially inhibits breast cancer cell growth and invasiveness,		
CC	while not affecting the growth of non-tumour cells. Yeast SPL		
CC	is used in a claimed method for identifying agents that modulate		
CC	SPL activity. SPL inhibitors will inhibit growth of cancer cells,		
CC	especially breast cancer cells. SPL inhibitors, including		
CC	polynucleotides preventing expression of SPL genes, or antibodies		
CC	against SPL, can also be used to prevent the development and/or		
CC	metastasis of cancer, especially where the inhibitor is linked to an		
CC	antitumour or antioestrogen receptor antibody. Detection of		
CC	alterations in an endogenous SPL sequence can be used to diagnose		
CC	cancer, and to assess the prognosis for recovery.		
XX			
XX	Sequence 589 AA:		

Query Match 33.8%; Score 1007.5; DB 20; Length 589;
 Best Local Similarity 39.1%; Pred. No. 4.9e-89;
 Matches 209; Conservative 108; Mismatches 185; Indels 33; Gaps 12;

QY 51 LLIVWGIEF-----VFQPESL---WSRFKKCKCFKLTTRKMPITIGRKIQDKLNTKTD 97
 D 60 LFVIFCYKLLISNFEYLLKVGVPVRLAVRTYEHSRRRLFRLDLPFLRGTVKEKEVTVKQ 119
 QY 98 DISKMSFLVKDKKEYK--ALPSGGLSSAVLEKLEKYSM--DAFQEGRASGTVYSGE 153
 D 120 SIEDEL--IRSDSOLMNPOLPSPNGIPQDDVIELNKLNDLIPHTQMEGKGVSAVYHGG 177
 QY 154 EKTLELLVKAAGDFWMSNPLHPDIFPGLRIEAEIVRIACSLFNGGPD--CGCVTSQGT 212
 D 178 DDLIHLOTIAVEKVCVANOHLHPDVFPAVRKMESEVSVMLRMFAPSDTCGCTTSSGTE 237
 QY 213 SILMACKACRDLA--EKGITPEIYAPQSAHAENKAASYGKMTIVRPL--TKMMEVDYR 270
 D 238 SLILACLSAKMYALHNGITETPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQYDVG 297
 QY 271 AMRAISRNTAMLCSTFPPFPHGVIDPVEPAKLAAYKKIPLHYDACLGFLIFMEKAG 330
 D 298 KVKKEFKKNTLLVGSAPNPFHGIADIEGLGKTAQRYKPLPHVDSCLSGSEIYVFMKAG 357
 QY 331 YPLEHPDFRYKGVTSISADTHKGYAPKGSLLVYSDKKYRNYQFVDTDMOGGIYASP 390
 D 358 YKNLPDLDFRVPGVTSISCDTHKGYAPKGSVIMYRNSDLRMHQYVYNPMTGGLYGP 417
 QY 391 TIAGSRPGISACMAALMHGENGVEATKQIIKTA--RFLKSELENIKGIYFVGNPOLS 449
 D 418 TLGASRGAIVYGCWATVMVNGENGYIESCOEIVGAAMKFKKYIOENIPDLNINGNPRYS 477
 QY 450 LIALGSRDFDIYRLSNIMTAKGWLNLQOPPSIHFCITLLHARKRAVLOFLKRIRESVT 509
 D 478 VISFSSKTLNHEISDRLSKGMHFNALQKVPALHMAFTRLISAH---VDEICILRTTV 534
 QY 510 QIMK--NPKAKTTGMAIYMAQTVDRNNVAELSSVFLDSL---STDVTVO 557
 D 535 QELKSESNKSPDGTSAIVGAGSVKTAGVADKLIVGFLDALYKLGEGEDTATK 589

RESULT 12
 AAG70706
 ID AAG70706 standard; Protein: 589 AA.
 XX
 AC AAG70706;
 XX
 DT 27-JUL-2001 (first entry)
 XX
 DE S cerevisiae apoptosis associated protein YDR294C.
 XX
 KW Yeast; fungus; apoptosis; infection; proliferative disease;
 KM vaccine; autoimmune disease; ischaemia; neurodegeneration.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN W0200102550-A2.
 XX
 PD 11-JAN-2001.
 XX
 PF 03-JUL-2000; 2000MO-BE00077.
 XX
 PR 01-JUL-1999; 99EP-0870141.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Contreas RH, De Backer MD, Luyten WHML, Malcorps IKL;
 XX
 PI Nelissen BJM, Reekmans RJ,
 XX
 DR WPI: 2001-367042/38.
 DR N-PSDB: AAH29742.
 XX

PT Yeast and fungal nucleic acids encoding proteins involved in a pathway
 PT leading to programmed cell death, useful for treating proliferative
 PT disorders, yeast and fungal infections, or for preventing apoptosis in
 PT certain diseases -

XX Claim 1; Fig 1; 218pp; English.

XX The present invention provides the protein and coding sequences of a
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*
 CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify
 CC treatments for fungal and yeast infections, for proliferative diseases
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
 CC and neurodegeneration. The present sequence is one of the *S. cerevisiae*
 CC proteins of the invention.

XX Sequence 589 AA;

Query Match 33.8%; Score 1007.5; DB 22; Length 589;
 Best Local Similarity 39.1%; Pred. No. 4.9e-89;
 Matches 209; Conservative 108; Mismatches 185; Indels 33; Gaps 12;

QY 51 LLIVWGIEF-----VFQPESL---WSRFKKCKCFKLTTRKMPITIGRKIQDKLNTKTD 97
 D 60 LFVIFCYKLLISNFEYLLKVGVPVRLAVRTYEHSRRRLFRLDLPFLRGTVKEKEVTVKQ 119
 QY 98 DISKMSFLVKDKKEYK--ALPSGGLSSAVLEKLEKYSM--DAFQEGRASGTVYSGE 153
 D 120 SIEDEL--IRSDSOLMNPOLPSPNGIPQDDVIELNKLNDLIPHTQMEGKGVSAVYHGG 177
 QY 154 EKTLELLVKAAGDFWMSNPLHPDIFPGLRIEAEIVRIACSLFNGGPD--CGCVTSQGT 212
 D 178 DDLIHLOTIAVEKVCVANOHLHPDVFPAVRKMESEVSVMLRMFAPSDTCGCTTSSGTE 237
 QY 213 SILMACKACRDLA--EKGITPEIYAPQSAHAENKAASYGKMTIVRPL--TKMMEVDYR 270
 D 238 SLILACLSAKMYALHNGITETPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQYDVG 297
 QY 271 AMRAISRNTAMLCSTFPPFPHGVIDPVEPAKLAAYKKIPLHYDACLGFLIFMEKAG 330
 D 298 KVKKEFKKNTLLVGSAPNPFHGIADIEGLGKTAQRYKPLPHVDSCLSGSEIYVFMKAG 357
 QY 331 YPLEHPDFRYKGVTSISADTHKGYAPKGSLLVYSDKKYRNYQFVDTDMOGGIYASP 390
 D 358 YKNLPDLDFRVPGVTSISCDTHKGYAPKGSVIMYRNSDLRMHQYVYNPMTGGLYGP 417
 QY 391 TIAGSRPGISACMAALMHGENGVEATKQIIKTA--RFLKSELENIKGIYFVGNPOLS 449
 D 418 TLGASRGAIVYGCWATVMVNGENGYIESCOEIVGAAMKFKKYIOENIPDLNINGNPRYS 477
 QY 450 LIALGSRDFDIYRLSNIMTAKGWLNLQOPPSIHFCITLLHARKRAVLOFLKRIRESVT 509
 D 478 VISFSSKTLNHEISDRLSKGMHFNALQKVPALHMAFTRLISAH---VDEICILRTTV 534
 QY 510 QIMK--NPKAKTTGMAIYMAQTVDRNNVAELSSVFLDSL---STDVTVO 557
 D 535 QELKSESNKSPDGTSAIVGAGSVKTAGVADKLIVGFLDALYKLGEGEDTATK 589

RESULT 13
 AAG70849
 ID AAG70849 standard; Protein: 589 AA.
 XX
 AC AAG70849;
 XX
 DT 27-JUL-2001 (first entry)
 XX
 DE C albicans apoptosis associated protein #29.
 XX
 KW Yeast; fungus; apoptosis; infection; proliferative disease;
 KM vaccine; autoimmune disease; ischaemia; neurodegeneration.
 XX
 OS Candida albicans.
 XX

PN WO200102550-A2.
 XX 11-JAN-2001.
 XX 03-JUL-2000; 2000WO-BE00077.
 XX 01-JUL-1999; 99EP-0870141.
 XX (JANC) JANSEN PHARM NV.
 XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
 PI Nelissen BJM, Reekmans RJ;
 XX WPI: 2001-367042/38.
 DR N-PSDB; AAH2985.
 XX
 XX Yeast and fungal nucleic acids encoding proteins involved in a pathway
 PT leading to programmed cell death, useful for treating proliferative
 PT disorders, yeast and fungal infections, or for preventing apoptosis in
 PT certain diseases -
 XX
 XX Claim 24: Fig 2; 218pp; English.
 XX
 XX The present invention provides the protein and coding sequences of a
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*
 CC cerevisiae and the fungus *Candida albicans*. These can be used to identify
 CC treatments for fungal and yeast infections, for proliferative diseases
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
 CC and neurodegeneration. The present sequence is one of the *C. albicans*
 CC proteins of the invention.
 XX
 XX Sequence 589 AA:

Query Match 31.9%; Score 949; DB 22; Length 589;
 Best Local Similarity 37.0%; Pred. No. 2,6e-83;
 Matches 217; Conservative 107; Mismatches 202; Indels 60; Gaps 18;

OY 9 LKAFPPYLET---LEVSTKAKNYVNGH-CTKPYMOLIAMSVVWTL-----IYWGE 58
 DB 18 LTKLKYQLKILFLATYCAQSGFGLNGSVCLARD---IFGVYVYTLKLYRYLRGYG 74
 OY 59 FVFGPESLW---SREKKKFKLTRKMPILIGRKIDDKLTKTDIDSKNMSFLKVDKEYK 114
 DB 75 IYDSIRRLKLYVSVSSQIFSLPRISKIDKELATIGKVEELMKN-----DPQLQ 128
 OY 115 --ALPSSGLSSAV--LEKLEKXSSMDAFWQEGRASGVYSGEKLTELKAYGADPAW 169
 DB 129 FPELEGGIDADNVSLELDKLNKLKHD--WINGRVSGAVYHGENLSTLQVEAYKKYSV 186
 OY 170 SNPLHDPLEPGRIKTEKIVRIACSLFNGGPDSCCVSGSTESTILMACKACROLAFE-K 228
 DB 187 ANQLHPDVFPGVKMEAEVHVHVDIFNAPSDCGSGTSGTESILLGLSAREYKKRYR 246
 OY 229 GIKPPEIYVPOSAHAFAFKKASYFGMKIVRVPLTKM-NEVDVRRARRAISRTATLVYST 287
 DB 247 GITEEVYLAPTIINGIEKACEYFGMKLHKVDLPVTQVYDKKVERLINSTVITLIGSA 306
 OY 288 POFPHGVIDPVEVAKLAVKKYKIPLVHDACTGGLIVMEKA-----GYPLEHDFR 341
 DB 307 PNYPGIIDIESTELKAVKYNIPLVHDACTGSLFVLEKSKVHGDRKLP---FDRPL 363
 OY 342 KGVTSISADTRKHYGAPRGSSLYVSDKKRYNOYQFVTDWOGGIYASPTLAGSRPGGS 401
 DB 364 PGVVISCDTRKHYGAPRGSSITIMRSPLKRECOYIYASDWTGMYGSPTLAGSRPGALV 423
 OY 402 AACAAALHFGENGVEATEKQIITKARFLAKSELEN---IKGIFVFGNPLSLIL----- 453
 DB 424 VGCATLNLNKGKGTTCFCYDVSAMKVKRAIETDPLSKHLQITGPISGIVISFQLAP 483
 OY 454 -GSRDEDIYRLSNLTAKGWLNLQPPPSIHFCITLLHARRKVAIQPLKIDRESVOTIM 512
 DB 484 OOSGNLSIYEISDLTKKGMHFAATLQNSALHFAFTRILTV--PVDDELIALDVEATKEAV 541

OY 513 -----KNPKAKTIG-MGAIYMAQTYDVMNVALLSSVFIDSLY 550
 DB 542 AIAEHKKNKGVTKAPGDTAIGIAGSVHTAGLADRLIYAFIDTLY 587
 RESULT 14
 ID AAB96568 standard; Protein; 384 AA.
 XX AAB96568;
 AC AAB96568;
 XX 29-OCT-2001 (first entry)
 DT Putative P. abyssal glutamate decarboxylase.
 XX Hyperthermophilic archaeon; hyperthermophilic protein.
 KM Pyrococcus abyssi.
 OS Pyrococcus abyssi.
 XX FR2792651-A1.
 PN 27-OCT-2000.
 PD 21-APR-1999; 99PR-0005034.
 PF 21-APR-1999; 99PR-0005034.
 XX 21-APR-1999; 99PR-0005034.
 PR (CNRS) CNRS CENT NAT RECH SCI.
 PA (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX Forterre P, Thiery JC, Prieur D, Dietrich J, Lecompte O;
 PI Querellou J, Weissenbach J, Saurin W, Heilig R;
 XX WPI: 2001-126236/14.
 DR New nucleotide sequences isolated from *Pyrococcus abyssi* encode
 XX proteins useful in industry -
 PT
 PT Claim 7; Pages 1298-1300; 1657pp; French.

The present invention relates to the genomic sequence of *Pyrococcus*
 CC abyssi (see AAF6431 and AAH4123-7) and P. abyssi proteins. P. abyssi is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade.
 CC Note: This patent is in the same patent family as WO200065062, which
 CC contains additional sequences as shown in AAB9132-AAB99143,
 CC AAH75903-AAH75920 and AAG66436.
 CC
 XX Sequence 384 AA:

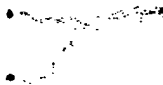
Query Match 17.3%; Score 514.5; DB 22; Length 384;
 Best Local Similarity 30.6%; Pred. No. 3.9e-41;
 Matches 121; Conservative 86; Mismatches 164; Indels 25; Gaps 7;

OY 117 PSQGLSSAVLEKLEKXSSMDAFWQEGRASGVYSGEKLTELKAYGADPAWNP LHPD 176
 DB 5 PEKGLPREVLELRLDKTRKVDLTSSGKILGSMCMTPH---ELAIEVARYIDRLGDPG 61
 OY 177 IFPGIKTEAEIVRIACSLFNGGPDSCCVSGSTESTILMACKACROLAFEKIGITPREY 236
 DB 62 LHPGTRKIEEVEIEMLSDLH-LEKGYGHIVSGTEAMILAVARRNIS--DAERPELI 117
 OY 237 APOSAHAFAFKKASYFGMKIVRVPLTKMNEVDVRRARRAISRTATLVYSTPOPHGVYD 296
 DB 118 LPKSAHFSTIAGEMLVKYLWMAELKODYADVVKVEAKISDNTIGIYIAGTGLGYVD 177
 OY 297 PVEVYAKLAVKKYKIPLVHDACTGGLIVMEKAGYRLEPHDFRKYGVTSIADTRKHYG 356
 DB 178 DIPALSDLABREGIDPLHVDAGFVLPFAKSLGYDLP-DFDFKLGKGVSTIIDHKKGM 236

QY 357 APMGSSVLVYSGKKYRNYQFVDTWOGGIYASPTIAGSRPGISACMAALMHFGENGY 416
D 237 APIPAGGIIFRRKKYLAISVLAGKWKWQATITGRGASVLAVMALIKHLEGEY 296
QY 417 VEATKQIKTARFLKSLLENKGFVGNQSLIAGSRPDIYRLSNMTAKGMNLN- 475
D 297 REIVRKMEISRWAEIKRLNNAVLREPLNIVSFQTK--NLKVERELKRGWGISA 354
QY 476 -----QLQPPPSIHFCITLLHARKRVAIOFLKDIRE 506
D 355 HRGYIRIVFMP-----HVKKEVVEELRDIRE 381
RESULT 15
AAV15212
ID AAV15212 standard; Protein: 76 AA.
AC AAV15212;
XX 26-OCT-1999 (first entry)
DE Sphingosine-1-phosphate lyase homologue fragment amino acid sequence.
XX
KM sphingosine-1-phosphate; sphingosine-1-phosphate lyase; SPHINGLY;
KM G-protein coupled receptor; EDG-1; secondary messenger; cancer;
KM cardiovascular disorder; thrombosis; atherosclerosis; wound healing;
KM stroke; apoptosis; homologue; fragment; ds.
XX
OS Homo sapiens.
XX
FH key
FT MISC-difference 42 Location/Qualifiers
FT MISC-difference 44 /note= "encoded by NTC"
FT MISC-difference 48 /note= "encoded by NAA"
FT MISC-difference 62 /note= "encoded by NAT"
FT MISC-difference 63 /note= "encoded by ATN"
FT MISC-difference 70 /note= "encoded by GNC"
FT MISC-difference 70 /note= "encoded by NAT"
XX
PN MO938983-A1.
XX
PD 05-AUG-1999.
XX
PF 24-DEC-1998; 98WO-EP08564.
XX
PR 03-NOV-1998; 98GB-0024026.
PR 29-JAN-1998; 98EP-0300625.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Godden RJ, Testa TT;
XX
DR WPI; 1999-479192/40.
DR N-PSDB; AA206343.
XX
PT A new sphingosine-1 phosphate lyase useful for diagnosing and
PT treating cancers, cardiovascular disorders, thrombosis or
PT atherosclerosis
XX
PS Claim 18; Page 24; 37pp; English.
XX
CC This is the amino acid sequence of the Sphingosine-1-phosphate
CC lyase homologue fragment. The lyase catalyses the cleavage of
CC sphingosine-1-phosphate to give a long chain aldehyde and
CC phosphoethanolamine.
CC The sequence has use as a method of treating cancers, cardiovascular
CC disorders, thrombosis, atherosclerosis and other conditions. This is due
CC to the action of sphingosine-1-phosphate intracellularly as a secondary

CC messenger and extracellularly as a ligand for the G-protein coupled
CC receptor EDG-1.
XX
SQ Sequence 76 AA:
QY 467 MTAKGMNLNQLQPPPSIHFCITLLHARKRVAIOFLKDIRESVIOIMKPKATTGMCAIY 526
D 1 MTAKGMNLNQLQPPPSIHFCITLLHARKRVAIOFLKDIRESVITKIMKPKATTGMCAIY 60
QY 527 AMAQTVDKRVVDEL 541
D 61 GIDQTVDRNVGRI 75

Search completed: October 6, 2003, 13:49:46
Job time : 52 secs



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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:39:24 ; Search time 57 Seconds
(without alignments)
2571.472 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MPSTDLMKAFEPYLEILE.....LYSTDPIYVQSGQNMNGSPKPH 568

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	2959	99.4	580	4	Q9UG68
2	2950	99.1	568	4	Q95470
3	2567	86.2	568	11	Q8CHN6
4	2557	85.9	568	11	Q8ROX7
5	2553	85.8	568	11	Q54955
6	2551	85.7	568	11	Q8C942
7	1344	45.1	545	5	Q9V772
8	1082	36.3	552	5	Q9Y194
9	1069	35.9	544	10	Q9C509
10	1052	35.3	576	3	Q8X074
11	1025	34.4	557	10	Q93V78
12	1008	33.9	542	5	Q17456
13	1007.5	33.8	589	3	Q05567
14	882	29.6	606	5	Q966E7
15	669	22.5	488	17	Q28946
16	621.5	20.9	414	17	Q27989

17	567.5	19.1	454	17	Q9Y9M1	Q9Y9M1 aeropyrum p
18	549.5	18.5	473	17	Q9Y6B1	Q9Y6B1 aeropyrum p
19	518.5	17.4	383	17	Q58679	Q58679 pyrococcus
20	514.5	17.3	384	17	Q9UZD5	Q9UZD5 pyrococcus
21	511	17.2	371	17	Q8U1P6	Q8U1P6 methanobact
22	482	16.2	363	17	Q27188	Q27188 methanosarc
23	422	14.2	398	17	Q8PYX5	Q8PYX5 methanosarc
24	393.5	13.2	395	17	Q8TU09	Q8TU09 methanosarc
25	380	12.8	367	17	Q28275	Q28275 archaeoglob
26	337	11.3	372	17	Q8TV92	Q8TV92 methanopyru
27	315	10.6	468	17	Q8TPG4	Q8TPG4 methanosarc
28	308.5	10.4	464	17	Q9HS43	Q9HS43 halobacteri
29	269	9.0	464	16	Q8XIO6	Q8XIO6 clostridium
30	258.5	8.7	125	10	Q8LEF9	Q8LEF9 arabidopsi
31	253.5	8.5	460	16	Q06249	Q06249 mycobacteri
32	244	8.2	500	10	Q9AR41	Q9AR41 cryza sativ
33	239.5	8.0	304	16	Q8YBJ0	Q8YBJ0 bruceella me
34	237.5	8.0	489	16	Q8FNG5	Q8FNG5 escherichia
35	234.5	7.9	464	2	Q8GFI5	Q8GFI5 edwardsiell
36	233.5	7.8	496	10	Q81102	Q81102 nicotiana t
37	230.5	7.7	514	3	Q9UV77	Q9UV77 aspergillus
38	230	7.7	494	10	Q944L6	Q944L6 arabidopsi
39	229.5	7.7	496	10	Q8LKR4	Q8LKR4 nicotiana t
40	229.5	7.7	520	3	Q8XOB0	Q8XOB0 neurospora
41	228.5	7.7	496	10	Q81101	Q81101 nicotiana t
42	226.5	7.6	496	10	Q9AT17	Q9AT17 nicotiana t
43	225.5	7.6	496	10	P93369	P93369 nicotiana t
44	225	7.6	419	10	Q8RXH0	Q8RXH0 arabidopsi
45	217.5	7.3	467	16	P73043	P73043 synechocyst

ALIGNMENTS

RESULT 1
Q9UG68 PRELIMINARY; PRT; 580 AA.
ID Q9UG68
AC Q9UG68; Q9UN89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA1252 (Sphingosine-1-phosphate lyase)
DE (EC 4.1.2.27) (Fragment).
GN KIAA1252 OR SPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
RN [2]
RP SEQUENCE OF 13-580 FROM N.A.
RA Zhou J., Saba J.;
RT "Cloning and characterization of human sphingosine-1-phosphate lyase
RT gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -I- CONFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL: AB033078; BAA6566.1; -;
DR EMBL: AF144638; AAD44755.1; -;
DR GeneW. HGNC:10817; SGP.L1.
DR InterPro: IPR002129; Pyridoxal-dec.
DR Pfam: PF00282; Pyridoxal-dec; 1.
KW Hypothetical protein; Decarboxylase; Lyase; Pyridoxal phosphate.
FT NON_TER 1 1

SQ SEQUENCE 580 AA: 64961 MW: 7B18137B02DA65C9 CRC64;
 Query Match 99.4%; Score 2959; DB 4; Length 580;
 Best Local Similarity 99.5%; Pred. No. 1.1e-242;
 Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEFV 60
 |||||
 DB 13 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEFV 72
 |||||
 QY 61 FQPELSMSRFRKKCFELTRKMPILIGRKIDDKLTKTDIDSKNNSFLKVKVEYKALPSOG 120
 |||||
 DB 73 FQPELSMSRFRKKCFELTRKMPILIGRKIDDKLTKTDIDSKNNSFLKVKVEYKALPSOG 132
 |||||
 QY 121 LSSSAVLEKLEKSSMDAFMOEGRASGTYSGEKEKTELLVYKAYGDFAMSNPLHPDIFPG 180
 |||||
 DB 133 LSSSAVLEKLEKSSMDAFMOEGRASGTYSGEKEKTELLVYKAYGDFAMSNPLHPDIFPG 192
 |||||
 QY 181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKAYRDLAEKGIKTPETIAPQS 240
 |||||
 DB 193 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKAYRDLAEKGIKTPETIAPQS 252
 |||||
 QY 241 AHAFAFKKASFGMKIVRPVPLTKMMEVDVRAHRRAISRNTAMLCSTPQPHGVDPVE 300
 |||||
 DB 253 AHAFAFKKASFGMKIVRPVPLTKMMEVDVRAHRRAISRNTAMLCSTPQPHGVDPVE 312
 |||||
 QY 301 VAKLAVKRYKIPLVHVDACLGFLIVEMKAGYPLEHFDPRVKVTSISADTHKYGAPRG 360
 |||||
 DB 313 VAKLAVKRYKIPLVHVDACLGFLIVEMKAGYPLEHFDPRVKVTSISADTHKYGAPRG 372
 |||||
 QY 361 SSLVLYSDKKRYNYCFEVDTDWQGIYASPTIAGSRPGISAAWMAALMHFGENGVEAT 420
 |||||
 DB 373 SSLVLYSDKKRYNYCFEVDTDWQGIYASPTIAGSRPGISAAWMAALMHFGENGVEAT 432
 |||||
 QY 421 KOIITARPLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 480
 |||||
 DB 433 KOIITARPLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 492
 |||||
 QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAE 540
 |||||
 DB 493 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAE 552
 |||||
 QY 541 LSSVFLDSLSTDTVTYQSGQMNGSPKPH 568
 |||||
 DB 553 LSSVFLDSLSTDTVTYQSGQMNGSPKPH 580
 |||||

RESULT 2
 095470
 ID 095470 PRELIMINARY; PRT; 568 AA.
 AC 095470;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
 DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20471968; PubMed=11018465;
 RA Van Veldhoven P.P., Gijssbers S., Mannaerts G.P., Vermeesch J.R.,
 Brys V.;
 RT "Human sphingosine-1-phosphate lyase : cDNA cloning, functional
 expression studies and mapping to chromosome 10q22.";
 RL Biochim. Biophys. Acta 1487:128-134(2000).
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
 TYRDC).
 DR EMBL: AJ011304; CAA09590.2; -;
 DR Interpro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec; 1.

KW Decarboxylase; Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 568 AA: 63491 MW: 113CFAD4F6C41AA CRC64;
 Query Match 99.1%; Score 2950; DB 4; Length 568;
 Best Local Similarity 99.3%; Pred. No. 6.1e-242;
 Matches 564; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEFV 60
 |||||
 DB 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEFV 60
 |||||
 QY 61 FQPELSMSRFRKKCFELTRKMPILIGRKIDDKLTKTDIDSKNNSFLKVKVEYKALPSOG 120
 |||||
 DB 61 FQPELSMSRFRKKCFELTRKMPILIGRKIDDKLTKTDIDSKNNSFLKVKVEYKALPSOG 120
 |||||
 QY 121 LSSSAVLEKLEKSSMDAFMOEGRASGTYSGEKEKTELLVYKAYGDFAMSNPLHPDIFPG 180
 |||||
 DB 121 LSSSAVLEKLEKSSMDAFMOEGRASGTYSGEKEKTELLVYKAYGDFAMSNPLHPDIFPG 180
 |||||
 QY 181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKAYRDLAEKGIKTPETIAPQS 240
 |||||
 DB 181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKAYRDLAEKGIKTPETIAPQS 240
 |||||
 QY 241 AHAFAFKKASFGMKIVRPVPLTKMMEVDVRAHRRAISRNTAMLCSTPQPHGVDPVE 300
 |||||
 DB 241 AHAFAFKKASFGMKIVRPVPLTKMMEVDVRAHRRAISRNTAMLCSTPQPHGVDPVE 300
 |||||
 QY 301 VAKLAVKRYKIPLVHVDACLGFLIVEMKAGYPLEHFDPRVKVTSISADTHKYGAPRG 360
 |||||
 DB 301 VAKLAVKRYKIPLVHVDACLGFLIVEMKAGYPLEHFDPRVKVTSISADTHKYGAPRG 360
 |||||
 QY 361 SSLVLYSDKKRYNYCFEVDTDWQGIYASPTIAGSRPGISAAWMAALMHFGENGVEAT 420
 |||||
 DB 361 SSLVLYSDKKRYNYCFEVDTDWQGIYASPTIAGSRPGISAAWMAALMHFGENGVEAT 420
 |||||
 QY 421 KOIITARPLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 480
 |||||
 DB 421 KOIITARPLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 480
 |||||
 QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAE 540
 |||||
 DB 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAE 540
 |||||
 QY 541 LSSVFLDSLSTDTVTYQSGQMNGSPKPH 568
 |||||
 DB 541 LSSVFLDSLSTDTVTYQSGQMNGSPKPH 568
 |||||

RESULT 3
 08CHN6
 ID 08CHN6 PRELIMINARY; PRT; 568 AA.
 AC 08CHN6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Van Veldhoven P.P.;
 RT "Comparison of sphingosine-1-phosphate lyases.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ512838; CAD55407.1; -;
 KW Lyase.
 SQ SEQUENCE 568 AA: 63758 MW: A0B59A072CC79F48 CRC64;
 Query Match 86.2%; Score 2567; DB 11; Length 568;
 Best Local Similarity 85.2%; Pred. No. 2.3e-209;
 Matches 463; Conservative 36; Mismatches 48; Indels 0; Gaps 0;

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QY 1 MSTDLLMLKAFEPYLEILEYVSTKAKNVNCHCTKEPWOIAMSVMVTLIIYGEYEV 60
DB 1 MSTDLLMLKDFEPELEILEYVSTKAKNVNCHCTKEPWOIAMSVMVTLIIYGEYEV 60
QY 61 FOPESLMSRFKKKCKFLTRKMPITIGRKIQDKLNTKTDISKMSFLKYDKREYKALPSQG 120
DB 61 FOPESLMSRFKKKCKFLTRKMPITIGRKIQDKLNTKTDISKMSFLKYDKREYKALPSQG 120
QY 121 LSSAVLEKLEKESMDAFWQEGRASGVTSGEKLTLLKAYADDFAMSNPLHDPDPPG 180
DB 121 LSTAEVLEKLEKESMDAFWQEGRASGVTSGEKLTLLKAYADDFAMSNPLHDPDPPG 180
QY 181 LKTEAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDALFEKIGITPELIVAPQS 240
DB 181 LKTEAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDALFEKIGITPELIVAPQS 240
QY 241 AHAAPNKAASYFGMKIVAVPLTKMMEVDVRAKRAISBNTAMLVCSFQPPHGVDPPE 300
DB 241 AHAAPNKAASYFGMKIVAVPLTKMMEVDVRAKRAISBNTAMLVCSFQPPHGVDPPE 300
QY 301 VAKIAVKKIPLHDACGGLIYVMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
DB 301 VAKIAVKKIPLHDACGGLIYVMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
QY 361 SSVLVSDKKYRNVOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHGECNGYVAT 420
DB 361 SSVLVSDKKYRNVOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHGECNGYVAT 420
QY 421 KOIKTARFLKSELENKIGIFVGNPQLSIALGSRDPDIYRLSNLMTAKGNLNLQLOFP 480
DB 421 KOIKTARFLKSELENKIGIFVGNPQLSIALGSRDPDIYRLSNLMTAKGNLNLQLOFP 480
QY 481 PSIHFCITLLARKKVAIOFLKDIRESTQIMKNKAKTTGMAIYAAQTTVDNRVAE 540
DB 481 PSIHFCITLLARKKVAIOFLKDIRESTQIMKNKAKTTGMAIYAAQTTVDNRVAE 540
QY 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567
DB 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567
QY 541 ISSVFLDSLSTDTVTOGSONMGSPKP 567
DB 541 ISSVFLDSLSTDTVTOGSONMGSPKP 567

RESULT 4
Q8ROX7 PRELIMINARY: PRT: 568 AA.
AC Q8ROX7:
DB 01-JUN-2002 (TREMBlrel. 21, Created)
DB 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DB 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DB Sphingosine phosphate lyase 1.
DE Sphingosine phosphate lyase 1.
GN SGP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver:
RA Strausberg R.;
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.*;
CC Nature 420:563-573(2002).
CC -1 COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (PDC, GAD, HDC AND
CC TYRDC).
DB EMBL: BC026135; AAH26135.1; -.

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DR EMBL: AK036747; BAC29562.1; -.
DR EMBL: AK037789; BAC29872.1; -.
DR EMBL: AK049342; BAC33695.1; -.
DR MGD: MGI:1261415; Sgpl1.
DR InterPro: IPR002129; Pyridoxal_dec.
DR Pfam: PF00282; Pyridoxal_dec; 1.
KW Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 568 AA; 63677 MW; FASD52E4EF9D09E CRC64;

Query Match      85.9%; Score 2557; DB 11; Length 568;
Best Local Similarity 84.3%; Pred. No. 1.6e-208;
Matches 478; Conservative 43; Mismatches 46; Indels 0; Gaps 0;

QY 1 MSTDLLMLKAFEPYLEILEYVSTKAKNVNCHCTKEPWOIAMSVMVTLIIYGEYEV 60
DB 1 MSTDLLMLKDFEPELEILEYVSTKAKNVNCHCTKEPWOIAMSVMVTLIIYGEYEV 60
QY 61 FOPESLMSRFKKKCKFLTRKMPITIGRKIQDKLNTKTDISKMSFLKYDKREYKALPSQG 120
DB 61 FOPESLMSRFKKKCKFLTRKMPITIGRKIQDKLNTKTDISKMSFLKYDKREYKALPSQG 120
QY 121 LSSAVLEKLEKESMDAFWQEGRASGVTSGEKLTLLKAYADDFAMSNPLHDPDPPG 180
DB 121 LSSAVLEKLEKESMDAFWQEGRASGVTSGEKLTLLKAYADDFAMSNPLHDPDPPG 180
QY 181 LKTEAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDALFEKIGITPELIVAPQS 240
DB 181 LKTEAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACRDALFEKIGITPELIVAPQS 240
QY 241 AHAAPNKAASYFGMKIVAVPLTKMMEVDVRAKRAISBNTAMLVCSFQPPHGVDPPE 300
DB 241 AHAAPNKAASYFGMKIVAVPLTKMMEVDVRAKRAISBNTAMLVCSFQPPHGVDPPE 300
QY 301 VAKIAVKKIPLHDACGGLIYVMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
DB 301 VAKIAVKKIPLHDACGGLIYVMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
QY 361 SSVLVSDKKYRNVOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHGECNGYVAT 420
DB 361 SSVLVSDKKYRNVOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHGECNGYVAT 420
QY 421 KOIKTARFLKSELENKIGIFVGNPQLSIALGSRDPDIYRLSNLMTAKGNLNLQLOFP 480
DB 421 KOIKTARFLKSELENKIGIFVGNPQLSIALGSRDPDIYRLSNLMTAKGNLNLQLOFP 480
QY 481 PSIHFCITLLARKKVAIOFLKDIRESTQIMKNKAKTTGMAIYAAQTTVDNRVAE 540
DB 481 PSIHFCITLLARKKVAIOFLKDIRESTQIMKNKAKTTGMAIYAAQTTVDNRVAE 540
QY 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567
DB 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567
QY 541 ISSVFLDSLSTDTVTOGSONMGSPKP 567
DB 541 ISSVFLDSLSTDTVTOGSONMGSPKP 567

RESULT 5
Q54955 PRELIMINARY: PRT: 568 AA.
AC Q54955:
DB 01-JUN-1998 (TREMBlrel. 06, Created)
DB 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DB 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DB Sphingosine-1-phosphate lyase (EC 4.1.2.27).
DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).
GN SGP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=96125521; PubMed=9464245;
RA Zhou J., Saba J.D.;
RT Identification of the first mammalian sphingosine phosphate lyase

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Db 186 LLSKETASGGQICGNTSGTESIVLAVSSRDYMKKGTREPMIIPESGHSAYDKA 245
QY 249 ASYEGMKIVRPLTKMEVDVRAAMRAISRNTAMLCVSTPOEPHGVIDPVEVAKLVKY 308
Db 246 AQFVKIKMRYPVVKDRADYKATRRHINRTIMIVGSAPEFGIITDPIELGQALSY 305
QY 309 KIPLVADACGLFVIVEMERAGYLEHPFERVGVNISADTHKGYAPKSSLVLYSD 368
Db 306 GICHHVDCGLGFLVLPARKIGYQIP-PFDSVGVGISIVDVHKYGLAPRGSTVLYRN 364
QY 369 KKRNYOPFVDTMOGGIIVASPTIAGSRPGGISAACNAALMHGSENGVEATKOIITAR 428
Db 365 HEIKHOFVAVTEWMSGGLYVSPITAGSRPGSLVAGAAWAMSLGEEGYLQNTSKIMEASK 424
QY 429 FLKSELNKGIFVFGNRPQSLIALGSRDPIYRLSLMTAKGNLNLQLOPPSIHFCIT 488
Db 425 RLEGVREIHELFEYIGPMDITVAFGSKALDIEFVNDIMSSKGWHLNALOPNSIHICIT 484
QY 489 LLMARKKVAIOFLKDIESVTOIMKNPKAKTTGCAIYAMAQTVDRNMVAELSSVFLDS 548
Db 485 LGHY--PVVDLFMDLREAVETVKANPGITGGLAPIYGAAKMPDGMVVELLVFMDS 542
QY 549 LY 550
Db 543 QY 544

RESULT 10
08X074 ID 08X074 PRELIMINARY; PRT; 576 AA.
AC 08X074;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Probable sphingosine-1-phosphate lyase.
GN B14D6.540.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC)
DR EMBL; AL356173; CAB91763.2; -
DR InterPro; IPR001092; HLH_Basic.
DR InterPro; IPR002129; Pyridoxal_dec.
DR Pfam; PF00282; Pyridoxal_dec.1.
DR PROSITE; PS00038; HLH.1; 1.
KW Decarboxylase; lyase; Pyridoxal phosphate.
SQ SEQUENCE 576 AA; 63519 MW; EDFZCDB323BB41A7 CRC64;

Query Match 35.3%; Score 1052; DB 3; Length 576;
Best Local Similarity 41.9%; Pred. No. 1.6e-80;
Matches 224; Conservative 115; Mismatches 154; Indels 42; Gaps 16;

QY 49 WTLIIWVG-----YEVFQPEISMSRKKCFKLTAKMPLIGKRIQDKLTKTODISK- 101
Db 49 WTRRALMKLKGRLGFLFE---LFTDARILYGFYFLRPGVRRKVRQADID---DALTKM 102
QY 102 NMSFLKVDKEXVKALPSQGLSSAVLEKLEKYSMD-AFQWEGRGAIVYSGEKEITELL 160
Db 103 QAKKIPACQIRYLSLPKRGWTEAVRKLELALMTDHTRWSDGYSGAVVSGEDELKQLQ 162
QY 161 VKAYGDFAMSNPLHPDIFPGLRKIEAIVRIACSLFNGGPDSCGCVTSGTESIIMACKA 220

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Db 163 TEAYGKFTVANPIHPDVEPGVRKMEAEVVAVLISLFNAPPGAAVSTSGTESIIMAILS 222
QY 221 CRDLAF-EKGKTEPEIYAPOSAHAFKKAASYFEK--YRVPLTKMEVDVRAAMRAIS 277
Db 223 AROKAYHERGVTEEMIIPEYAHAFKRAEYFNKIKHLVACP-APTYOVDTKVVARILN 281
QY 278 RNTAMLCVSPQFPHGVIDPVEVAKLVAKKIPDLHYDACGLFVIFMEKAGYLEHPF 337
Db 282 RNTIMLVGSAPNPFHGIIIDISALSKLAKRKIPDLHYDACGLFVIFMEKAGYLEHPF 340
QY 338 DFRVKGVTISADTHKGYAPKRGSSLVLYSDKKRYNOFVDTMOGGIIVASPTIAGSRP 397
Db 341 DFRKGVTSISCDHKKGFAPKNGSVLYRAELRSYQYFVDPMSGSGVYASPGIAGSRP 400
QY 398 GGISAACWALMHGSENGVEATQOIT---KTRFLKSELENIKGFVGNPQLSLIAL 453
Db 401 GALTAACWASLMSYGEGBYLSCTQIYGATRKLEHIRSHPTLQOELEILNPLVSVLAF 460
QY 454 GSR-DPDIYRLSNLMTAKGNLNLQLOPPSIHFCITLLHAR--KRAVIOFLKDI----- 504
Db 461 QARGDLNITYDIADGMSRGMHLNLQNPRAIHAVTAPVAKNMERLA-QDEGVVEERE 519
QY 505 RESVTQIM-----KNPKAKTTG-MGAIYAMAQTVDRNMVAELSSVFLDSLY 550
Db 520 KERVOYEALKMGISGKTGKOKAGDTAALYGVAGSLPNKSVVVDLARGFLDLLY 574

RESULT 11
093VF8 ID 093VF8 PRELIMINARY; PRT; 557 AA.
AC 093VF8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative sphingosine-1-phosphate lyase.
GN P0672D08.7 OR P0402A09.4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0672D08."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0402A09."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
DR EMBL; AP003727; BAB64236.1; -
DR EMBL; AP003610; BAB62623.1; -
DR InterPro; IPR002129; Pyridoxal_dec.
DR Pfam; PF00282; Pyridoxal_dec.1.
KW Decarboxylase; lyase; Pyridoxal phosphate.
SQ SEQUENCE 557 AA; 60536 MW; C21CEC1B7BD6198 CRC64;

Query Match 34.4%; Score 1025; DB 10; Length 557;
Best Local Similarity 39.5%; Pred. No. 3e-78;
Matches 223; Conservative 103; Mismatches 190; Indels 48; Gaps 12;

QY 22 YSTRAKNVNCHCTKYPEWOLIAWSVYVTL--IYGVFVQPEISMSRKKCFKLTAR 79

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Db      3 FALRLDAAHHLSRYEPLVLLAALLAARLTHAAAAAVALDRGLRTVLLALANTAIK 62
Qy      80 KMPIIGRKIQDLINKTKDID-----SKNMSFLVKDEKYVALPSSGLSSAVLEKLEKYES 135
Db      63 LEPGSAYINAKRKRVVDQLOSGGSTSTKLTRE-----LPTVGLSNG-VINDELTAK 115
Qy      136 MNAFQEGASGTVY----SGEKLLELVKAYGDFAWSPNPLHPDIFPGILRKIEAEIVRIA 192
Db      116 RQVNMQ-GKSCSTVYIAGSESEGHFALINKAYSMESHPLQDVHFKSVAOLEAEVYVAMT 174
Qy      193 CSLF-----NGPDSGCVTSGSTESILMACACRD-LAFKGIKTPETVAPOSAAAN 246
Db      175 AALLGTRKESSGGQICGNMTSGCTESILAVTSDYMTKKGITKPEMILAESASAYD 234
Qy      247 KAASYFGMKIVRVPPLTKMEVDVRAMRAISRNTALVYSTQFPFGVIDPVEYAKLAV 306
Db      235 KAAQGFNIKVRVPVAKPEFLADYKGFRCINGNTIMVGSAPGPRGLDPIBELGELAS 294
Qy      307 KKIPLHVDACIGCFIYVMEKAGYPLEHPDPFRKCVTSISADTHKYGYAPKGSGLVY 366
Db      295 RDICLHVDLCGGEVLPFARKLGYPID-PDFECVKGVTISSTDVHKYGLAPKGTISVLY 353
Qy      367 SSKKYY-----NQGFVD-----TDMOGIYASPTIGSRPRGTSAC 404
Db      354 KHEIRKISWLSLHNTYSLTDMIMQNTKMFQYEMTGLVSEFTIAGSRPGULIAGA 413
Qy      405 MAALMHFENGVEATKQIITARFLKSELENIKGIFVGNPOLSLIALSGRDFIYRLS 464
Db      414 WAAWSTSLGNGYEMNTGHMEVSKIQRIEDIPGLFVIGKPDMTYVAGSSVDLFEVN 473
Qy      465 NIMTKAGNNLQLOPPSIHFCITLLHARKVAQLFQKDIRESVTOIMKPKAKTTGMA 524
Db      474 DIMSSGWHNLQSPNSLHICVTLOHT--VIYEELKDLKDSVDVTKANPGPISGGRAP 531
Qy      525 IYAAQTVDRMVAELSVFLDS 548
Db      532 IYGAAGKMPDRGMRELLVEFMDA 555

RESULT 12
017456 PRELIMINARY; PRT: 542 AA.
AC      017456:
DT      01-NOV-1996 (Tremblrel. 01, Created)
DT      01-NOV-1996 (Tremblrel. 01, last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, last annotation update)
DE      Hypothetical 61.1 kDa protein.
GN      B0222.4
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OX      Rhabditidae; Pelodermidae; Caenorhabditis.
RN      NCBL_TaxID=6239;
RP      SEQUENCE FROM N.A.
RC      STRAIN-Bristol N2;
RX      MEDLINE=9069613; PubMed=9851916;
RA      None;
RT      Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology. The C. elegans Sequencing Consortium.
RT      Science 287:2012-2018 (1998).
RL      [2]
RN      SEQUENCE FROM N.A.
RC      STRAIN-Bristol N2;
RT      Du 2., Gattung S.;
RT      "The sequence of C. elegans cosmid B0222.";
RL      Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Bristol N2;
RA      Waterston R.;
RT      "Direct Submission.";
RL      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC      -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

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CC      -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC      TYRDC).
DR      EMBL: U50312; AAA92321.1; -.
DR      Wormpep: B0222.4; GE06699.
DR      Interpro: IPR002129; Pyridoxal_dec.
DR      Interpro: IPR006025; Zn_MTPeptide.
DR      Pfam: PF00282; pyridoxal_dec; 1.
DR      PROSITE: PS00142; ZINC_PROTEASE; 1.
KW      Hypothetical protein; Decarboxylase; Lyase; Pyridoxal phosphate.
SQ      SEQUENCE 542 AA; 61133 MW; 3EB9A3082A8A426 CRC64;

Query Match      33.9%; Score 1008; DB 5; Length 542;
Best Local Similarity 38.1%; Pred. No. 8, 1e-77;
Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

Qy      19 LEVYSSTAKNNYNGCHTKYEPQQLAWSVWMLLIYWGVEFVEFQEPESLSRKKCKFKLT 78
Db      5 LEQYHS-AKDLIFELRKNPVLYVSTIVATVYVTLNLRHMLHDEKIKRLSTVEFTTV 63
Qy      79 KMPIIGRKIQDLINKTKDIDISKNMSFLVKDEKYVALPSSGLSSAVLEKLEKYESMDA 138
Db      64 KRVPIFKMKIDQLNEVDKLEKSLRTVDRSTYEFTTISHSVGREYRLAAYIDDLG 123
Qy      139 -FWQGRASGTVYSGEKL--TELLKAYGDFAWSPNPLHPDIFPGILRKIEAEIVRIASL 195
Db      124 PAFLGGRVSGAVFNRDDKDEREMEYEGKFAWNPPLPKLFPGRIMEAEVVMCCNM 183
Qy      196 FNGSPDSCCVSSGGSESTLMACKCRDLAFKGIKTPETVAPOSAAHAFKNAASYFGMK 255
Db      184 MNGDSETCGTSTGGISILLACLARHNLRLRGEYTEMIPVSSVHAAFFAAACFRK 243
Qy      256 IYRVPLTKM-MEVDVRAMRAISRNTAMLVYSTQFPFGVIDPVEYAKLAVKRIPLHY 314
Db      244 VKKIPDVPTEFVLDYKMAALINKRQCMVGSAPEPPEGTVDIEIGLGLEYDIPHY 303
Qy      315 DACLGGLFVMEKAGYPLEHPDPFRKCVTSISADTHKYGYAPKGSGLVLYSKKRYNY 374
Db      304 DACLGGLFLPLEED---EIRYDERVPPVSSISADSHKYGGLAPGSSVVALRNNLELHN 359
Qy      375 QFEVPTDMOGIYASPTIGSRPGTSACMAALMHFENGVEATKQIITARFLKSEL 434
Db      360 QTFCDADMOGGIYASATMGSRAGHNNIALCMAAMLVHAGCKAANAKKIVDTTKIRNGL 419
Qy      435 ENIKGIFVGNPOLSLIALGSRD-FDIYRLSNLMTAKGNNLQLOPPSIHFCITLLHAR 493
Db      420 SNIKGIKLOGPDSQVCSWTNDGVELYEFHFMKEKHQNLGLOFPAGVHIWMTMNTGH 479
Qy      494 KRVAIOFLKDIRESVTOIM--KNPKAKTTGMAQITVDRMVAELSVFLDSLYS 551
Db      480 PELAEAFVADCRAAVEFYKSHKPSSEDKTSEAIYGLAOSIPDRSLVHEFAHSYIDAVYA 539

RESULT 13
005567 PRELIMINARY; PRT: 589 AA.
AC      005567:
DT      01-NOV-1996 (Tremblrel. 01, Created)
DT      01-NOV-1996 (Tremblrel. 01, last sequence update)
DT      01-OCT-2002 (Tremblrel. 22, last annotation update)
DE      Similar to glutamate decarboxylase.
GN      DPL1 OR D9819.5 OR YDR294C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
RN      NCBL_TaxID=4932;
RP      SEQUENCE FROM N.A.
RC      STRAIN-S288C;
RA      Fulton L.;
RL      Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-S288C;

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RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favello A., Fulton L., Gattung S., Greco T., Kitzman J., Kucaba T.,
 RA Hallworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menzies S.,
 RA Miller N., Nhan M., Pauley A., Peluso D., Riken L., Riles L.,
 RA Talch A., Trevisan E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.,
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RL Waterston R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA Jia Y., Cherry J.M.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
 DR EMBL: U51031; AAB64470.1; -;
 DR SCD; S0002702; DPL.
 DR Interpro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec; 1.
 KM Decarboxylase; Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 589 AA; 65565 MW; 75FAF8182AF72266 CRC64;

Query Match 33.88; Score 1007.5; DB 3; Length 589;
 Best Local Similarity 39.14; Pred. No. 1e-76;
 Matches 209; Conservative 108; Mismatches 185; Indels 33; Gaps 12;

51 LLIWVGEF-----VFPESL-----WSRKKCKFKLRKMPITGRKIOKLNKTGD 97
 DB LEVIFCKLISNFFYLKIVGVPLAVRTYEHSSRLFRMLDSPFLRGTEKEVTKVKQ 119
 QY 98 DISKNSFLKVDKEYV--ALPSQGLSSAVLEKLEKESM--DAFQEGRASGTVYSGE 153
 DB 120 STDEL--IRSDSQLNFPQLPSNGIPQDDVIEELNKLNLGHTQKEKVGAYVHG 177
 QY 154 EKTLLVKAYGDPANSPNLPDIPFGLRKIEAEIVRIACSLFNGSPDS--CGCVTSGETE 212
 DB 178 DDILHLOTIYERKVCVANOQLHPDVPFVPRKMESEVSMVLRMFNAPSDTGCSTTSGTE 237
 QY 213 SILMKACGRDLAF--EKGITPELVAPOSAAHAFNAASVFGKIYAVPL--TKMEVDVR 270
 DB 238 SLLACLSAKMYALHNRGITPELVAPOSAAHAFNAASVFGKIYAVPL--TKMEVDVR 297
 QY 271 AMRRASIRNTAMLVCSFPPCPHGVIDPVEPAKLAAYKIPILHVADCLGFLIVEMKAG 330
 DB 298 KVKKFKINKNTILLVGSAPNRPFGIADIEGLKIAQKYLPLHVDSCLGSEFIVSFMKAG 357
 QY 331 YPLEHPDFRYKCVTISADTHKYGVA PKGSSLVLYSDKKYRNYQFQVDTWOGGIYASP 390
 DB 358 YKMLPLDFRPVPTGISCTHRYGFA PKGSSVIMYNSDLRMHQYVNPAMTGGIYGP 417
 QY 391 TINGSPRGISAAQMALMHFENGVEATKQIITKA--RELKSELEIKIKIIFPGNPOLS 449
 DB 418 TLGSRGATLVGCGMAYVMGNGEYTESCEETVGAAMKFKYIODEIPLNTMGNGRYS 477
 QY 450 LIALGSRDPDIYRLSNLTAKGNLNLQDPFPPSHFCITLLHARKRVAIOFLKDIRESVT 509
 DB 478 VIFSSKTLNHLHSDRLSKKGMFNALOKRVALHMFRLSAH---VDEIDCLILRTIV 534
 QY 510 QIMK---NPKAKTTGKATYAMAQTYVDRMVAELSSVFLDSL---STDTVTO 557
 DB 535 QEIKSESNSKSPDGSATLVAGVSVTAGVADKLIVGFLDALYKILGPGEDTATK 589

RESULT 14
 Q966E7 PRELIMINARY; PRT; 606 AA.
 AC Q966E7;
 AC Q966E7;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein Y104H12D.3.
 GN Y104H12D.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology." The C. elegans Sequencing Consortium.
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Bauer C., Courtney L., Maupin R.;
 RT "The sequence of C. elegans cosmid Y104H12D.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Waterston R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
 DR EMBL: AC006701; AAK68403.2; -;
 DR WormRep: Y104H12D.3; CE31632.
 DR Interpro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec; 1.
 KM Hypothetical protein; Decarboxylase; Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 606 AA; 68135 MW; 4A79F8D4340975CC CRC64;

Query Match 29.64; Score 882; DB 5; Length 606;
 Best Local Similarity 34.68; Pred. No. 5e-66;
 Matches 185; Conservative 116; Mismatches 204; Indels 30; Gaps 5;

31 NGCHTYEPQQLAMSVWTLIIWGYEFPQESLSRKKCFKLRKMPITGRKIOD 90
 DB 29 NACSGLEPQIYSAISLCLFLAYIKRMRSNRPVYQIKTFSRLSLPVRKRLTA 88
 QY 91 KLNKTYDDISKNNSFLKVDKEYVKAIPSGGLSSAVLEKLEKESM--DAFQEGRASGTVY 150
 DB 89 DLAKAQAEIDEVHOSDHMRFEYKFLPERCMTDEEILLADGRRYAM----- 134
 QY 151 SGE-----EKTLELLVKAYGDFPMSNPLHPDIPRGIRKIEAEIVRIACSLFNG 198
 DB 135 -GERRRYQHYDPOTREDMKLSAKLFDLFANHPDHRSDAPFGKMEAEILKMKCAFHG 193
 QY 199 GPSCGCVTSGGTESILMKACGRDLAEFGKITPELVAPOSAAHAFNAASVFGKIYR 258
 DB 194 GKSCGCVAGGCTEALMLACLAIRNRSRAGBRAEIVASTNHPALDKAAAFEDMTIKR 253
 QY 259 VPLTKME--VDVAMRRASIRNTAMLVCSFPPCPHGVIDPVEPAKLAAYKIPILHVAC 317
 DB 254 IOVSETDDBRANVAMKRAIRPTCMIIASAPNHITGVDPDIEKLAKLAQRHYHPLHVDCT 313
 QY 318 LGGFLIVEMKCAKAYPLEHPDFRYKCVTISADTHKYGVA PKGSSLVLYSDKKYRNYQF 377
 DB 314 LGGFLVLEPMYADYSVP--AFDFRLPVGTISADTHKYGQCPGRSLVLMYEPALRQF 372
 QY 378 VDTWOGGIYASPTIAGSRPGISAAQMALMHFENGVEATKQIITKA--RELKSELENI 437
 DB 373 TNSMPGCGYATPTMSGRGCGAVATPAMAMLLKRGYITNAORITTEAROLAYRLQGL 432
 QY 438 KGIFVGNPOLSLIAGSRDFDIYRLSNLTAKGNLNLQDPFPPSHFCITLLHARKRVA 497
 DB 433 DGVSIRGSDLCVAAFTSEVNVNIVDVAVQGMHVDPLSPAAARVPISLMCEGYL 492

QY 498 IOFLDIRESYTOIKKNPKAKTTGGA-IYANAQTTVDNRNMYAELSSVFLDLSYS 551
 DB 493 DHFLEDLMAICNLKSKMEPAEKIGTTASFYOMLQVNDKTLVDLSLRLAHYS 547

RESULT 15

O28946 PRELIMINARY; PRT; 488 AA.
 ID O28946
 AC O28946;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Group II decarboxylase.
 GN AF1323.
 OS Archaeoglobus fulgidus.
 OC Archaea: Euryarchaeota: Archaeoglobi: Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Fleischmann D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
 RA Kirtness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kalne B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RA "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -1- CORFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
 CC TYRDC).
 CC EMBL: AE001012; AAB89922.1; -.
 DR TIGR: AF1323; -.
 DR InterPro: IPR000463; Fatty_acid_BP.
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; Pyridoxal_dec; 1.
 DR PROSITE: PS00214; FAP; 1.
 KW Decarboxylase; Hypothetical protein; Lyase; Pyridoxal phosphate;
 KW Complete proteome.
 SQ SEQUENCE 488 AA; 54562 MW; 84AA3FOAE053CFB6 CRC64;

Query Match 22.5%; Score 669; DB 17; Length 488;

Best Local Similarity 36.5%; Pred. No. 4.6e-48;
 Matches 155; Conservative 83; Mismatches 171; Indels 16; Gaps 8;

QY 92 LNKTDIDSKMNSFLKVKVEYKALPSQGLSSAVLEKLEYSSMDAFWQEGRASGV-Y 150
 DB 10 LNKGGHNSFEVKYIRHTTRIMSPN-GSDAEGVLRLEDAKNDPEHSHRMWHIYY 68
 QY 151 SGEKLTLELVKAYGDFAMSNPLHPDIPPGLRKIEAIVRIAGSLFNGGPPDSCGCVTSGG 210
 DB 69 AGLKVVELARKAYIMYDMKTMLDPTCFPSLIMREYVMASSLLNGDEEYVGNFTYGG 128
 QY 211 TESILMAKACRDIAFEK--GIKTPETVAPQSAHAFAFNKAASYGKIVRPLTKMMEV 267
 DB 129 TESIMALKAAARE-KFRKEGGNVPELIVLPATAPAFWKSAYELGMCLRAKLDELRA 187
 QY 268 DYRAMRAISRKTAMLVCTSPQPHGVDPVPEVAKLAVKIKIPLHVDACLGGLIYME 327
 DB 188 DVEYKVELYGDKTAIVGSAIPNYPGVDIDIKALSDIAVDGKIMLHVADACLGGLIYME 247
 QY 328 KAGVLEHPDPFRVGVTSISADTFHKYKGYAPKGSLLVYSDKKYNNQFFVDTDMQGGIY 387
 DB 248 ELGEKIP-DFDSYVEGVHSHSADTFHKYGLSPGASVILLYRNNAKLREGQIFWASMPGYPL 306

QY 388 ASPTIAGSRPGGISACNAALMHFGENCYVEATKOIITARLKSLENINGIFVGNPQ 447
 DB 307 VNTAVLSTRSAGTILAAAWAVNSYLGFDGYLKLAKKTLVAKKRLIDGLTEL-GLLELGSPE 365
 QY 448 LSLIALGSRDDIYLSLMLTAKGNL-----NOLQFPFSIHFCITILLHAKKRAIOPFL 501
 DB 366 GAVLAFTSERHNLFEKVSITLMAEKGYVOSOPGSKLIGFPRSLHFSVIPGHA--EVDDEL 423
 QY 502 KDIRE 506
 DB 424 EDMRE 428

Search completed: October 6, 2003, 13:51:28
 Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:31:19 : Search time 19 seconds
(without alignments)
1405.851 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MSTDLMKAFEPYLEILE.....LYSTDVTVQSGQNGSPKPH 568

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369.5	12.4	396	1 Y050_METJA	Q60338 methanococ
2	261.5	8.8	466	1 DCE_LACIA	Q9CG20 lactococcus
3	258.5	8.7	466	1 DCE_LACIC	O30418 lactococcus
4	242	8.1	467	1 DCEC_LISIN	O32844 listeria in
5	236.5	7.9	466	1 DCEA_ECO57	P58228 escherichia
6	236.5	7.9	466	1 DCEA_ECOLI	P80063 escherichia
7	234	7.9	467	1 DCEC_LISMO	Q8Y4K4 listeria mo
8	233	7.8	500	1 DCE_PETHY	Q07346 petunia hyb
9	232.5	7.8	464	1 DCEB_LISMO	Q9EY49 listeria mo
10	230	7.7	502	1 DCEI_ARATH	O42521 arabidopsis
11	229.5	7.7	466	1 DCEB_ECOLI	P28302 escherichia
12	226	7.6	494	1 DCE2_ARATH	Q42472 arabidopsis
13	220.5	7.4	464	1 DCEB_LISIN	Q92849 listeria in
14	218.5	7.3	462	1 DCEA_LISMO	Q915P3 listeria in
15	209	7.0	502	1 DCE_LYCES	P54767 lycopersico
16	201.5	6.8	585	1 DCE_YEAST	O04792 saccharomyc
17	186	6.2	510	1 DDC_ACTIRA	Q43908 actinobact
18	178	6.0	511	1 DDC_HAETN	P71362 haemophilus
19	172	5.8	386	1 DCHS_VIBAN	Q96581 vibrio angu
20	156.5	5.3	377	1 DCHS_ENTAE	P81877 enterobacte
21	155.5	5.2	488	1 NFSI_CANAL	P87165 candida alb
22	151.5	5.1	405	1 DCHS_PSEFL	P95477 pseudomonas
23	150.5	5.1	434	1 Y610_METJA	Q58027 methanococ
24	149	5.0	495	1 RHBH_RHME	Q92371 rhizobium m
25	146.5	4.9	484	1 NFSI_CANMA	P87187 candida mal
26	144	4.8	369	1 DCHS_RHILLO	Q98A07 rhizobium 1
27	143.5	4.8	377	1 DCHS_MORMO	P05034 moronegella
28	141.5	4.8	377	1 DCHS_KLEPL	P28578 klebsiella
29	139	4.7	453	1 NFSI_ARATH	Q49543 arabidopsis
30	134.5	4.5	387	1 NFSI_RHISN	P35690 rhizobium s
31	132.5	4.5	404	1 ISCS_NEIMA	Q93960 neisseria m
32	132.5	4.5	410	1 ISCS_RICPR	Q92460 rickettsia
33	132	4.4	387	1 NIFS_RHOSH	Q01179 rhodobacter

34	131	4.4	451	1 NFSI_RAT	Q9939 ratius norv
35	131	4.4	585	1 DCE2_HUMAN	O05329 homo sapien
36	130.5	4.4	410	1 ISCS_RICCN	Q92461 rickettsia
37	130	4.4	585	1 DCE2_PIG	P48321 sus scrofa
38	129.5	4.4	451	1 NFSI_MOUSE	Q92133 mus musculu
39	129	4.3	391	1 AAT_PYROH	O58489 pyrococcus
40	129	4.3	497	1 NFSI_YEAST	P25374 saccharomyc
41	127	4.3	404	1 ISCS_NEIMB	Q93960 neisseria m
42	127	4.3	585	1 DCE2_MOUSE	P48320 mus musculu
43	127	4.3	585	1 DCE2_RAT	Q05683 ratius norv
44	126.5	4.2	488	1 GCS2_BACSU	P54377 bacillus su
45	126	4.2	1035	1 GCS2_SOLTU	Q49954 solanum tub

ALIGNMENTS

RESULT 1	ID	Y050_METJA	STANDARD:	PRT:	396 AA.
AC	Q60358:				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Hypothetical protein M0050.				
GN	M0050.				
OS	Methanococcus jannaschii.				
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;				
OC	Methanocaldococcaceae; Methanocaldococcus.				
OX	NCBI_TaxID=2190;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-JAL-1 / DSM 2661 / ATCC 43067;				
RA	MEDLINE=9633799; PubMed=868087;				
RA	Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,				
RA	Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,				
RA	Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,				
RA	Overbeek R., Kirkness E.F., Weinstock K.G., Fuhmann J.M., Glodok A.,				
RA	Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,				
RA	Uitterlisch T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,				
RA	Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,				
RA	Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;				
RT	"Complete genome sequence of the methanogenic archaeon, Methanococcus				
RT	jannaschii".				
RL	Science 273:1058-1073(1996).				
CC	-I- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,				
CC	GAD, HDC AND TYRDC).				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib.ch).				
CC	-----				
DR	EMBL; U67463; AAB98031.1; -				
DR	PIR; B64306; B64306.				
DR	TIGR; M0050; -				
DR	InterPro: IPR002129; Pyridoxal_dec.				
DR	Pfam: PF00282; Pyridoxal_dec; 1.				
KW	Hypothetical protein; Complete proteome.				
SO	SEQUENCE 396 AA; 45050 MW; 41CBBDEFA5ABBBC0 CMC64;				
Query Match	12.4%; Score 369.5; DB 1; Length 396;				
Best Local Similarity	27.9%; Pred. No. 1.9e-21;				
Matches 103; Conservative 82; Mismatches 139; Indels 45; Gaps 13;					
OY	113 VKALPSSGLSSAVLEKIKESMDAPWQBRASGTYISSEKTELTVKAYGFANSNP 172				
DB	1 MRNQEVSSEKLEIKRSLDLKEDNINGSNCSNVLPTTRITVDI--FLENTL 57				
OY	173 LHPDIFGLRIEAEIVRIACSLFNGPDSGCVTSGGTESIIMACACRDLAFKGIK- 231				

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Db      58 GDBGKGTLEEKVALLGSLN-NKDAYGHVSGTEANLALRCIKNIWREKRRG 116
Qy      232 -----TPETVAQSAHAFAFNKAASYGKRIVRPLTKMMEVDVRAARAISR---NTAM 283
Db      117 LSKNEHPRKIIVPTAFHFEKREMDLVIYAPIKEDTIDKFKADVEDVIGITG 176
Qy      284 VCSFQFPHGVDPPEVAKLAVKYPILHVDACLGFLIVEME---KAGYPLEHPDF 339
Db      177 IAGTTEL--GTIDNIEELSKIAKENNIYHVDAAFGLVIPFLDXXKKKG--VNYKDFE 232
Qy      340 RKGVATISADTHKGVYAKRGSILVXSOKKRYNPFVDTMOGSIYASP-----T 391
Db      233 SL-GVDSITIDPHKMGHCPIPSGGILFKDIGIKRY--LDVD-----APYLTERQAT 281
Qy      392 IAGSRPGISACMAALMHFGENGVEATKQIITKARFLKSELE--NIKIGFEVGNPQS 449
Db      282 IIGTRVFGGAGCTAVNLRRLGREGOKRYNECMENLYLKLENNFPIV---EPILN 338
Qy      450 LIALGSRDF 458
Db      339 IVAIEDEY 347

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RESULT 2

DCE_LACLA STANDARD; PRT; 466 AA.

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ID DCE_LACLA STANDARD; PRT; 466 AA.
AC 09CG20; 050645;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15) (GAD).
GN GADB OR LIL290.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-15, AND CHARACTERIZATION.
RC STRAIN=01-7;
RX MEDLINE=99337071; PubMed=10411264;
RA Nomura M., Nakajima I., Fujita Y., Kobayashi M., Kimoto H., Suzuki I.,
  Aso H.;
RT "Lactococcus lactis contains only one glutamate decarboxylase gene.";
RL Microbiology 145:1375-1380(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=2135186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarre K.,
  Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
  lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -1- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES
  THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE
  (By similarity).
CC -1- CATALYTIC ACTIVITY: L-glutamate + 4-aminobutanoate + CO(2).
CC -1- MISCELLANEOUS: The enzyme is maximally active at pH 4.7. The
  activity is stable at acidic pH values; there is no activity in
  the neutral pH range. At pH 4.1 the enzyme activity is retained
  at temperatures up to 70 degrees Celsius.
CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
  GAD, HDC AND TYRDC).
CC -----
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DR EMBL; AB010789; BAA24585.1; -
DR EMBL; AE006361; AAK05388.1; -
DR PIR; B66786; B66786.
DR InterPro; IPR002129; Pyridoxal_dec.
DR Pfam; PF00282; pyridoxal_dec.1
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 466 AA; 53926 MW; BDCD732253E473C2 CRC64;

```

Query Match

8 %; Score 261.5; DB 1; Length 466;

Best Local Similarity 23.0%; Pred. No. 7.2e-13; Mismatches 222; Indels 43; Gaps 13;

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Qy 116 LPSQGLSSAVLEKLEKESMDAFMOEGRASGVYSGEELTE-LLVKAYGDFWSPNPLH 174
Db 27 LPRYKLAQOSIERVAVYQVODMDENGNRLNLAFCQTYMPREAVKLSQLEKNAD 86
Qy 175 PDIFGLRKIEAIVRIACSLFENGSPDS--CGCVTSGTIESIIMA-----CKACRDL 224
Db 87 KSEYPRTEIENRCVMNIADLNMASERKFMGTSTIGSEACWLGGMANKFSWRKRAERL 146
Qy 225 AFEKGIKTPETIYVQSAHAFAFNKAASYFGKRIVRPLTK-MMEVDVRAARAISRMT--- 280
Db 147 GIDINAKKPNLVISGTYQWCEKFCITYMDIEMREYPMDEHMSINLDKMDYVDEYTG 206
Qy 281 --AMLYCSTPQEPH-GVIDPVEVAKLAVKYPILHVDACLGFLIVEMKAGYPLEHPF 337
Db 207 VGIMGITTYGRDDIKALDNLIEYVKQTDYKYYHVDASGLVAFVEP-----ELDM 261
Qy 338 DFRVACVTSISADTHKYGAPKGSILVYSKKRYNPFVDTMOGSIYASFTTASRSP 397
Db 262 DFRKLVNISINTSGHYGLVPGVGVWLMDKKYLEPEELIFYVSYLGDELPTMAINFHS 321
Qy 398 GGISACMAALMHFGENGVEATKQIITKARFLKSELENIKGFVNGN--POLSLAL-- 453
Db 322 ASOLIGQYTNFVRYGDSYKAIHERHYKAMFLAKIEK-TGFEIEMNGSOLPTVYKL 380
Qy 454 --GSRDFDIYRLSNMTAKGMNLNQLPPPSI-HECITLILNAR---KRVAIQFLKDR 505
Db 381 KEDSNRGMWLYDLADLMLKGMQVPAYPLPKNLNENIQLRVIRADFGNMAMPNYQDMQ 440
Qy 506 ESYTQIMK-----NPKAKTTG 521
Db 441 EAIEALNKAHILYHEEPENKTYG 463

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RESULT 3

DCE_LACLC STANDARD; PRT; 466 AA.

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ID DCE_LACLC STANDARD; PRT; 466 AA.
AC 030418;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15).
GN GADB.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=MG1363;
RX MEDLINE=98143417; PubMed=9484886;
RA Sanders J.W., Leenhouts K., Burghoorn J., Brands J.R., Venema G.,
  Kok J.;
RT "A chloride-inducible acid resistance mechanism in Lactococcus lactis
  and its regulation."
RL Mol. Microbiol. 27:299-310(1998).
CC -1- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES
  THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE.
CC -1- CATALYTIC ACTIVITY: L-glutamate + 4-aminobutanoate + CO(2).
CC -1- CORFACTOR: Pyridoxal phosphate (By similarity).
CC -1- INDUCTION: EXPRESSION IS HIGHEST AT ONSET OF STATIONARY PHASE IN

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CC PRESENCE OF NAEL AND GLUTAMATE, AND AT LOW PH. CHLORIDE-DEPENDENT
CC EXPRESSION IS ACTIVATED BY GADR.
CC SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TYRDC).
CC -----
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CC -----
DR EMBL: AF005098; AAC46188.1; -
DR InterPro: IPR002129; Pyridoxal.dec.
DR Pfam: PF00282; Pyridoxal.dec.1.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
FT BINDING 277 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 466 AA; 53849 MM; 28894EB3FEEB16BD C64;

Query Match 8.7%; Score 258.5; DB 1; Length 466;
Best Local Similarity 22.3%; Pred. No. 1.2e-12;
Matches 101; Conservative 74; Mismatches 215; Indels 63; Gaps 12;

QY 116 LPSGLSSAVLEKTEKREYSSMDAFWQEGRASGVYSGEKLTE-LLYKAYGDFAWMSPLH 174
DB 27 LPRKKLAQOSIEPRVAQVODVDEMLDEGNARLNATFCQTYMEPEAKYKMSQTEKNAID 86
QY 175 PDIFPGJRKTEAEIVRIACSLFNGGPS--CGCVTSGETESILMA-----CKACRDL 224
DB 87 KSEYPRTEIEINRCVNMADLMANSEKGIYGTSTIGSSACMLGAMKRFWSWRRAEKL 146
QY 225 AFEKGITPELVAAQSAHAANKAASYFGMKIVRPLTKMNEVDVRRAMRAISRNTAMLV 284
DB 147 GLDINAKKPNLVISGYOVCEKFCVYWDIEMREVPMD-----REHMSINLEKVM 196
QY 285 CSTQPPHGVY-----DVPPEVAKLAVKKKPIPLHVADACGGFLIVPE 327
DB 197 DYVDEYITGVGIMGITTYGKYDIDKALDNLIEYKNOTDKYVYIHDAASGGLYAPVE 256
QY 328 KAGYPLEHPEDFRVKGVTISADTHKYGYAPKSSLVLYSDKKYRNYQFVDTMGGIY 387
DB 257 P-----ELENDFRLKNVYSINTSGHKYGLVYPGVWVLMRKYLPPELLIKYVSLGEL 311
QY 388 ASPIIASSRPGISAAACMAALMHGNGYVATKOIITANFLKSELENIGIVFGN-- 445
DB 312 PTMAINFHSASQILIGQYNEFVRGFGDYKAIHERTHVAMYLAEIEK--TGMEIINDG 370
QY 446 POLSLIAL-----GSRFDIYRLSNLMTAKGMNLNQLQFPSI--HFCITLHAR----KR 495
DB 371 AQLPIVCYKLEKNSRGNLIDLDRLMLKMGVYANPLPKNLENIQRLVIRADGGMN 430
QY 496 VALQFLADIRESVTQINK-----NPKAKTTG 521
DB 431 MAFNYVODMGEAIDALNKAHLFQEPENKTYG 463

RESULT 4
DCEC_LISTIN STANDARD; PRT; 467 AA.
AC 0928K4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probab1 glutamate decarboxylase gamma (EC 4.1.1.15) (GAD-gamma).
GN L1N2528.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;

RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Delhou P.,
RA Domann E., Dominguez-Bernal G., Duchud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez S., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurpkat G.,
RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjati H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Trieretz A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RA "Comparative genomics of *Listeria species*,"
RL Science 294:849-852(2001).
CC -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TYRDC).
CC -----
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CC -----
DR EMBL: AL596172; CAC97755.1; -
DR PIR: AC1748; AC1748.
DR Listlist: L1N02528;
DR InterPro: IPR002129; Pyridoxal.dec.
DR Pfam: PF00282; Pyridoxal.dec.1.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 467 AA; 53690 MM; 008AB18FE274590 C64;

Query Match 8.1%; Score 242; DB 1; Length 467;
Best Local Similarity 20.4%; Pred. No. 2.4e-11;
Matches 100; Conservative 92; Mismatches 222; Indels 76; Gaps 15;

QY 95 TKDISKMSF---LKVDEYKALPSQGLSSAVLEKREYSSMDAFWQEGRASGVY-- 149
DB 4 SENDKRHESIRIPLFSGSEESTSIPIKYLKKEPERIRIAQVYKVDQMDGMAQNAT 63
QY 150 --YGEERKTELVKAYGDFAMSNPLPDIFFGLRKIEAEIVRIACSLFNGGPS--CGC 205
DB 64 FQGYMEKEAEILM---AETLEKNAIDKSEYQJTAELNRCVNIADLMNPKMSYLG 120
QY 206 VTSGGTESILMACAC---RDLAFENKI---KTPLEVAQSAHAANKAASYFGMKIV 257
DB 121 STVGSSSEACMLGGLAMKFRMRNNAEKRLDIQARPNLIISSGYOVCEKFCVYWDVNR 180
QY 258 RVPLTK--MNEVDVRRAMRAISRNTAMLV-----CSTQPPH--GVIDVPPEVAKLAVKKI 310
DB 181 VVPMKDKHLSLDEKVEFLVDEYITGIVGILGITYGFDIALLDEVEVANEANHQ 240
QY 311 PLHVADACIGFLIVMEKAGYPLEHPEDFRVKGVTISADTHKYGYAPKSSLVLYSDK 370
DB 241 VIHIDGASGAMFTFVNP-----ELPMDFRLKNVYSINTSGHKYGLVYPGVWVLMRK 295
QY 371 YRNYQFVDTMGGIYASPIIASSRPGISAAACMAALMHGNGYVATKOIITANFL 430
DB 296 YLPKELFEVSYLDGSMPTMAINFSASQILIGQYNEFLRAGFGDYKAIHERTKYKTA 355
QY 431 KSELENIGIVFGN--POLSLIALGSRD-----FDIYRLSNLMTAKGMNLNQLQFPSI 483
DB 356 SKTYEK--SGYEIINDGSNLPIVCYKLDLDEYITGLYDLDQMLKMGVYANPLP--- 411
QY 484 HFCITLHARKRAVAIQFLKDIRSVTQINKPKAKTTGGAIVMAQTVDNRNVAELSS 543
DB 412 -----ADLSDTIIOF-----VCRADLGYNVAEEFAA 438

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OY      544 VFLLSLXSD 553
DB      439 DFADALHMLE 448

RESULT 5
DCEA_ECO57
ID      DCEA_ECO57      STANDARD:      PRT:      466 AA.
AC      P58228;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN      GADA OR GADS OR 24930 OR ECS4397.
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=83334;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX      MEDLINE=21074935; PubMed=11206551;
RA      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA      Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA      Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA      Grodeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
RA      Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA      Welch R.A., Blattner F.R.;
RT      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL      Nature 409:529-533(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / RIMD 050952;
RX      MEDLINE=21156231; PubMed=11258796;
RA      Hayashi T., Makino K., Kurokawa K., Ishii K., Yokoyama K.,
RA      Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA      Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA      Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT      "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT      O157:H7 and genomic comparison with a laboratory strain K-12.";
RL      DNA Res. 8:11-22(2001).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA (BY SIMILARITY).
CC      -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
CC      -1- CORACITOR: Pyridoxal phosphate (By similarity).
CC      -1- SUBUNIT: Homohexamer (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DPC,
CC      GAD, HDC AND TYRDC).
CC      -----
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: AE005577; AAG58658.1; -
DR      EMBL: AP002565; BAB37820.1; -
DR      PIR: E91178; E91178.
DR      PIR: F86024; F86024.
DR      InterPro: IPR002129; Pyridoxal_dec.
DR      Pfam: PF00282; pyridoxal_dec.
DR      PROSITE: PS00392; DDC-GAD-HDC_YDC. 1.
KW      Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family;
KW      Complete proteome.
FT      BINING      276      276      PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE      466 AA; 52699 MW; C7F9623DBB24F489 CR664;

Query Match      7.9%; Score 236.5; DB 1; Length 466;
Best Local Similarity      21.8%; Pred. No. 6,6e-11;
Matches      109; Conservative      86; Mismatches      206; Indels      99; Gaps      21;
OY      61 FQPSLMSRFKKKKL---TRKMPIIGRKIKDINKKIDISKMSFLKVDKE-YVAKL 116

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DB      9 FNSLDSRFGAALSTIAESKFP-----LHEMRDQV-----AFQIINDELIDGN 55
OY      117 PSQGLSSSAVLEKLEKSESSMDAFWQGRASGVYSGEKLTELVLKAYGDFAFMSNP LHPD 176
DB      56 ARQNLATPC-----QTWDD-----ENVHLMDSIN-----KNWIDE 88
OY      177 IFPGLEKIEAIVLRACSLF-----NGPDSGCVTSGGTESILMACAC-----RDL 224
DB      89 EYQSAIDRLRCVNMVADLMHAPAPKNG--QAVGTNTISSEACMLGAMKMRWRMRME 146
OY      225 AFEKKGKTEIYAPQSAHAFAFNKAASYFGMKIVRVPLTR-MNEVDVRAARRAISRATL 283
DB      147 AAGKPTDKPNLVC-CPVQICMHRFAKRYMDVELREIIPRGQLFMDKRMIEACDENTIGV 205
OY      284 V-----CSTPQFPGVVIDPVEVAKLWKKIPLHVNACGFLFIVMEKAGVYLEHP 336
DB      206 VPTFGVYTGNYEFPQPLDALDKF-QADTGIDIMHIDIAASGGLAFVAP-----DIV 259
OY      337 FDFRKGVTSISADTHKRYGAPKSSLVLYSDKKYNNYGFVDTMGGIYASPTIAGSR 396
DB      260 WDFRLPFRVKSISASGKFLGAPLPGCGVIMRDEEALPQLVFNVDYLGQIGTFAINFSR 319
OY      397 PGGISACMAALMHGSENGYVATKOIITARFLKSELENGIVF---GNPQLSLAL 453
DB      320 PAGQVIAQYEFRLRGREGYTVQNASYQVAAYLADEIAKL-GPYEICTGRDEGIPAV 378
OY      454 GSR-----DFDIYRLSMITAKGNLNLQLOFP-----PSIHFCITLLHARRKRAVIOF 500
DB      379 CERKKEGDEPGYTVLDLSERLRLRGH-----QVPATLGGEATDVIYMIKCRGEMDF 433
OY      501 ----LKDIRESVTQIMKNPK 516
DB      434 AELLLEDYKASLKYLSDHPK 453

RESULT 6
DCEA_ECOLI
ID      DCEA_ECOLI      STANDARD:      PRT:      466 AA.
AC      P80063;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN      GADA OR GADS OR B3517 OR C4328.
OS      Escherichia coli, and
OS      Escherichia coli O6.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562; 217992;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12;
RX      MEDLINE=92394884; PubMed=1522060;
RA      Smith D.K., Kassam T., Singh B., Elliott J.F.;
RT      "Escherichia coli has two homologous glutamate decarboxylase genes
RT      that map to distinct loci."
RL      J. Bacteriol. 174:5820-5826(1992).
RN      [2]
RP      SEQUENCE AND SEQUENCE OF 148-466 FROM N.A.
RC      STRAIN=ATCC 11246;
RX      MEDLINE=92155241; PubMed=1740158;
RA      Maras B., Sweeney G., Baria D., Bossa F., John R.A.;
RT      "The amino acid sequence of glutamate decarboxylase from Escherichia
RT      coli. Evolutionary relationship between mammalian and bacterial
RT      enzymes."
RL      Eur. J. Biochem. 204:93-98(1992).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12 / MG1655;
RX      MEDLINE=94316500; PubMed=8041620;
RA      Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT      "Analysis of the Escherichia coli genome. V. DNA sequence of the

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RT region from 76.0 to 81.5 minutes.";
 RL Nucleic Acids Res. 22:2576-2586(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-06.H1 / CFT073 / ATCC 700928;
 RX MEDLINE=2238823; PubMed=1247115;
 RA Resch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Skoch D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 RN [5]
 RP SEQUENCE OF 1-22.
 RX MEDLINE=94033862; PubMed=7764225;
 RA Yoshida T., Yamashino T., Ueguchi C., Mizuno T.;
 RT "Expression of the Escherichia coli dimorphic glutamic acid
 decarboxylases is regulated by the nucleoid protein H-NS.";
 RL Blost. Biotechnol. Blochem. 57:1568-1569(1993).
 RN [6]
 RP SEQUENCE OF 382-392.
 RC STRAIN-K12 / EWG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
 CC -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- SUBUNIT: Homohexamer.
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 GAD, HDC AND TYRDC).
 CC -1- DATABASE: NAME=worthington enzyme manual;
 WWW="http://www.worthington-biochem.com/manual/g/GUDP.html".
 CC -----
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 CC -----
 DR EMBL: M64024; AAA23833.1; -;
 DR EMBL: X63123; CAA44834.1; -;
 DR EMBL: U00039; AAB18493.1; -;
 DR EMBL: AE000428; AAC76542.1; -;
 DR EMBL: AE016768; AAN82764.1; ALT_INIT.
 DR PIR: S47737; S24234.
 DR ECO2DBASE: D046.5; 6TH EDITION.
 DR ECO2DBASE: E046.5; 6TH EDITION.
 DR EcoGene: EG50009; gada.
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC.1.
 KW Lyase; Decarboxylase; Pyridoxal phosphate; Multisene family;
 KM Complete proteome.
 FT BINDING 276 PYRIDOXAL PHOSPHATE.
 FT CONFLICT 64 C -> S (IN REF. 2).
 FT CONFLICT 73 H -> R (IN REF. 2).
 FT CONFLICT 153 D -> N (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 165 C -> S (IN REF. 2).
 FT CONFLICT 208 T -> N (IN REF. 2).
 FT CONFLICT 295 L -> V (IN REF. 2).
 FT CONFLICT 355 D -> N (IN REF. 2; AA SEQUENCE).
 SQ SEQUENCE 466 AA; 52685 MW; 86F963E710553E22 CRC64;

Query Match 7.98; Score 236.5; DB 1; Length 466;
 Best Local Similarity 21.88; Pred. No. 6.6e-11;
 Matches 109; Conservative 86; Mismatches 206; Indels 99; Gaps 21;

QY 61 FQPSLMSRRKKCKFKL--TRKPIIGRIQDKLNTKDDISKNSFLKYDKE-YVKAL 116
 Db 9 FRSELDLSRFGAKAISTIAESKRFP-----LHMERDVE-----AFQIINDELVDIGN 55
 QY 117 PSQGLSSAVLEKLEKKESSMDAFWQEGRASGVYSGEKKLTLLVKAAGPAMNPLHPD 176
 Db 56 ARONLAFFC-----QTWDD-----ENYHKMLDLSIN-----KNWIDKE 88
 QY 177 IFPELRRIEAEIVRIACSLF-----NGGPDSCGVSSGGESILTMCKAC-----RDL 224
 Db 89 EYFQSAIDLCRCVMVADLHMAPKNG--QAVGTNTIGSSSEACGLGMAMKMRKRME 146
 QY 225 AFEGKIRPEIYVAPQSAHAFAFNKAASYGKIVVPLTK-MNEVDVAMRRASIRNTAML 283
 Db 147 AAGKPTPKPNLYC-GPVOICMKHAKARWDELRIPIRPGOLFMDPRMIEACENTIGV 205
 QY 284 V-----CSTPQFPHGVIDPVEPVAKVAKYKIPLVNADCLGGLFLVFMKAGYPLEHP 336
 Db 206 VPTGVTYTGTYGVEPPQPLHDLAKF-QADYCIDIDMHIDAAGSGFLAFVAP-----DIV 259
 QY 337 FDFRVKGVTSISADTHKYGYPARKSSLYLVSDKKYRNVQFVDDMOGCIASPTIAGSR 396
 Db 260 WDFRLPRVKSTSASGHKFGALPAGCGWVIMDEBALPQELVFNVDYLGQGTALNFSR 319
 QY 397 PGGISACMAALMHFGENGVEATKQIITKARFLKSELENIGIFV---GNPOLSLIAL 453
 Db 320 PAGVIAQVYEFPLAGREGYTKKQNASYQVAAVLADELAKL-GYEFICTRPREGIPAV 378
 QY 454 GSR-----DFDIYRLSNLTAKGMNLQDP-----PSIHFCITLLHARRVAIQF 500
 Db 379 CFKLKDEDEPGYTYLDSERLRLRGW-----QVPAFTLGGRATDIVWRIMCRGFEWDF 433
 QY 501 ----LKDIRESVQIMKNPK 516
 Db 434 AELLLEDYKASLKYLSDPK 453

RESULT 7
 DCEC_LISMO
 ID DCEC_LISMO STANDARD; PRT; 467 AA.
 AC Q8Y4K4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Proba1 glutamate decarboxylase gamma (EC 4.1.1.15) (GAD-gamma).
 GN LMO2434.
 OS Listeria monocytogenes.
 ON Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Cherouani F., Couve E., de Darvar A., Deboux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Eshti H., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 CC -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 GAD, HDC AND TYRDC).
 CC -----
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CC -----
 CC EMBL: AL591983; CAD00512.1; -.
 CC PIR: AB1379; AB1379.
 CC ListList: LMO02434; -.
 CC InterPro: IPR002129; Pyridoxal_dec.
 CC Pfam: PF00282; Pyridoxal_dec.1.
 CC PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 CC Lysase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
 CC BINDING 278 278. PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC SEQUENCE 467 AA; 53640 MW; 6A48CB6FDC828BCF CRC64;

Query Match 7.9%; Score 234; DB 1; Length 467;
 Best Local Similarity 21.3%; Pred. No. 1e-10;
 Matches 100; Conservative 87; Mismatches 233; Indels 50; Gaps 15;

QY 95 TKDDISKNSF--LKVDEYVYKALPSQGLSSAVLEKLEYSSMDAFWQEGRASGV-- 149
 DB 4 SEDDKRQESYRIPFGSEESTSIPKYVKKPEPRAYQVLVDQLMDQGNARONLAT 63
 QY 150 --YSEBKTELIVAYGDFAANSPLHPDIFPGLEKIEAEYRIACSLFNGGPPDS--CCG 205
 DB 64 FCQTYMEKAEELIM--AETLEKNAIDKSEYPOTAELNRCVNIADLNNAPKDMSYLGT 120
 QY 206 VNSGSESTIMACKKC---RDLAPEKGI---KTPETIYAPQSAHAFAFKASVYGMKIV 257
 DB 121 STVGSESEACMLGGLMKFRMRNNAEKRGIDQAKRPNLISSGYOVCKFCVYMDVDR 180
 QY 238 RVPLETK-MMEVDVRAAMRAISRNTAMLV-----CSTPOEPH-GVIDPVEVAKLAVKYKI 310
 DB 181 VYPMKNNHLSLDVDFVDFDVTIGVVGIIIGITGTGKRDIDQLDEKVEAVNETNEHQL 240
 QY 311 PLHVACGLGFLIVMEKAGYPLEHPDPRVKGVSISADTKYGYAPRGSSLVLYSKK 370
 DB 241 VHIIDGASGAMFTPVNP---ELPMDERLKNVYSINSGHKYGYLVGVGMILMKDE 295
 QY 371 YNNOFVDTDMOGGIYASPTIAGSRPGGISAACMAALMHFGENGVEATKQIIKTARPL 430
 DB 296 YLPKELIPEVSYLGSMPTMAINFSRSQIIGQYINPLRYGFEGRREIHEKTKITATYL 355
 QY 431 KSELENKIGIEVFN--POLSLIALGSR---DFDIYRLSLMTAKGNLNLQLOPPSI 483
 DB 356 AKTVK-SGYFEIINDGANLPYVCYKMKEGLDVENTLYDLADQLMKGMQVAYPLPADL 414
 QY 484 HRCITLLHARK-----RVAIOFLKDIRESV-----TQIMKNPKAKTTGNG 523
 DB 415 SDTIQRFVYCRADLGYNVAEEFAADFAIDHNLHARHLYHDKERNDSYG 464

RESULT 8
 DCE_PETHY STANDARD; PRT: 500 AA.
 ID DCE_PETHY
 AC 007346;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutamate decarboxylase (EC 4.1.1.15) (GAD).
 GN GAD.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Petunia.
 OC NCBI_TaxId=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal;
 RX MEDLINE=93374956; PubMed=8366104;
 RA Baum G., Chen Y., Arazul T., Takatsujl H., Fromm H.:
 RT "A plant glutamate decarboxylase containing a calmodulin binding

RT domain. Cloning, sequence, and functional analysis.";
 RL J. Biol. Chem. 268:19610-19617(1993).
 CC -I- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
 CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
 CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
 CC BIOSYNTHESIS.
 CC -I- CATALYTIC ACTIVITY: L-glutamate + 4-aminobutanoate + CO(2).
 CC -I- COFACTOR: Pyridoxal phosphate.
 CC -I- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
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CC EMBL: L16797; AAA33709.1; -.
 CC PIR: A48767; AAA33710.1; -.
 CC DR EMBL: L16977; A48767.
 CC DR InterPro: IPR002129; Pyridoxal_dec.
 CC Pfam: PF00282; Pyridoxal_dec.1.
 CC PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 CC Lysase; Decarboxylase; Pyridoxal phosphate; Calmodulin-binding.
 CC BINDING 277 277. PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC FT DOMAIN 469 500. CALMODULIN-BINDING.
 CC SEQUENCE 500 AA; 56726 MW; 72A043CB885AE10D CRC64;

Query Match 7.8%; Score 233; DB 1; Length 500;
 Best Local Similarity 22.6%; Pred. No. 1.4e-10;
 Matches 104; Conservative 82; Mismatches 215; Indels 60; Gaps 15;

QY 92 LKKT--KDDISKNSFLKVDKEYKA-----LPQGLSSAVLEKLEYSSMDAFWQEG 143
 DB 3 LSKTYSQSVSHSIFA---SKYVRSILPRFKMPDINSITKEAYQIINDLMDGNRLN 59
 QY 144 RASGTVYSGEERTELIVKAYGDFAANSPLHPDIFPGLEKIEAEYRIACSLFNG---G 199
 DB 60 LASFTYTWMEPCDKLM---DSINKNVDMDEVPTTELOHRCVNMIAHFNAPLEDG 115
 QY 200 PDSGCGVSGTSTILMACKACRLAFE-----KGKTPETIYAPQSAHAFAFKNA 248
 DB 116 ETAVGAGVYGSSEALMLA---GLAFKRWONKKAKQKPCDKNITYGAVOVCEWF 170
 QY 249 ASYFGKIRVPLFTKMEV-DVRAAMRAISRNTAMLVSTPOEPHGVDPVEVAKLAVK 307
 DB 171 ARYFEVELKEVLSGGYVMDPEKAVEMVDENTICVAALISGLNGEPEDVARKLMDLVE 230
 QY 308 -----YKIPLVHVDACGLGFLIVMEKAGYPLEHPDPRVKGVSISADTKYGYAPGS 361
 DB 231 KKKETGMDPIHVDAASGFIAPFI---YF-ELEMDERLPLVKSINSGHKYGYLVGI 285
 QY 362 SLVYISDKKYRNYQFVDTDMOGGIYASPTIAGSRPGGISAACMAALMHFGENGVEATK 421
 DB 286 GNVVWRNKDDLPDELFIHINYLGAQDPFTTLNFSKSSGVIAQYQLRLGEGYKNWE 345
 QY 422 QIITKARFLKSELENKIGF-----VFGNPOSLLIALGSRDIDYRLSLMTAKGNLNLQ 476
 DB 346 NQENASVIRELEK-TGRFNISKEIGVPLVAFSLKDNKRONNEFISSTLRRFGIYVA 404
 QY 477 IQPPSIHFCITLLHA-----RKNVAIOFLKDIRESVTQI 511
 DB 405 YMPNNAQH-ITVLRAVIREDSRTLAERLVDIEKVLHEL 444

RESULT 9
 DCEB_LISMO STANDARD; PRT: 464 AA.
 ID DCEB_LISMO
 AC 09EYW9; 08Y450; 09AG00;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

RA Yoshida T., Ueguchi C., Yamada H., Mizuno T.;
 RT Function of the Escherichia coli nucleoid protein, H-NS: molecular
 RT analysis of a subset of proteins whose expression is enhanced in a
 RT hns deletion mutant".
 RL Mol. Gen. Genet. 237:113-122(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri, STRAIN=301 / Serotype 2a;
 RX MEDLINE=2272406; PubMed=12384590;
 RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao Y., Gao Y., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
 CC - CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
 CC - COFACTOR: Pyridoxal phosphate.
 CC - SUBUNIT: Homohexamer.
 CC - SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
 CC -----
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 CC -----
 DR EMBL: M84025; AAA23834.1; -
 DR EMBL: AE000245; AAC74566.1; -
 DR EMBL: D90791; BAA15163.1; -
 DR EMBL: D90790; BAA15157.1; -
 DR EMBL: AE005356; AAG56275.1; -
 DR EMBL: AP002557; BAB35521.1; -
 DR EMBL: X71917; CAA50736.1; ALT_SRO.
 DR EMBL: AE015194; AAN43309.1; ALT_INIT.
 DR PIR: B43332; B43332.
 DR PIR: B90891; B90891.
 DR PIR: G85726; G85726.
 DR EcoGene: EG11490; gadB.
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; Pyridoxal_dec.1
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC.1.
 DR Kasei: Decarboxylase; Pyridoxal phosphate; Multigene family;
 KW Complete proteome.
 FT BINDING 276 276 PYRIDOXAL PHOSPHATE.
 FT SEQUENCE 466 AA; 52668 MW; 8E65330A3C5BAED CRC64;
 SO
 Query Match 7.78; Score 229.5; DB 1; Length 466;
 Best Local Similarity 21.98; Pred. NO. 2.3e-10;
 Matches 108; Conservative 84; Mismatches 209; Indels 93; Gaps 20;
 OY 64 ELSMSRFKKKCFKLTFRKPIIGRKIDKLNKTKODISKNNKSPFLKYDKE-VYKALPQGLS 122
 DB 12 ELDSRRGAR-----SITLASKRPFLHMDRDV---AFQINDELTLIDGNARONLA 61
 OY 123 SSAVLEKLEKSSMDAFWQGRASGVYSGEKLTELLVAYAGDFPANSPLHPDIFPGLR 182
 DB 62 TFC-----QTWMD-----ENVNKLMDLSIN-----KNMIDKEEYQSA 94
 OY 183 KINAEIVRICSLF-----NGPDSGCVTSGCTESTIMACKAC-----RDIAFEKGI 230
 DB 95 AIDLRCNVAADLHMAPKNG--QAVGTNTIGSSSCMGMKMRMRKMEAAKPT 152
 OY 231 KPEIYVAPSAHAFAASVFGKIVRPFLTK-MMVVDVRAHRAISRTAMLY----- 284
 DB 153 DKRALVC-GPVQICMFKFAKRWDELREIPRPGQLMDPKRMLEACDENTIGVPTFGV 211
 OY 285 -CSTPQFPHGVIDPVEVAKLAVKYKIRPLHVDACLGFLVMEKAGYPLEHFPDPRVK 342

DB 212 TYTGNYEFPQPLHDLAKF-QADTGIDIDHIDAASGFLAFVAP-----DIWDFRLP 265
 OY 343 GVTISADTHKYGAPGSSLYLSDKKRYNFOFVTDMOGGIYAPPTAGSPGISA 402
 DB 266 RVKISASAGHKFGIAPGCGVWIRDEALPQELVFNVDYLGQIGFPAINFSPACQVI 325
 OY 403 ACNALHNGENGVEATKQIKTARFLKSELENKGFV-----GNPOLSLALGSR--- 456
 DB 326 AQYEFIRLREGYTKQNASYQVAAIYLADEIAKL-GPYEFICTGRPDEGIPAVCFKLD 384
 OY 457 ----DPIYRLSNIMTAKGNLNOLOPP-----PSIHFCITLLHARKRAIOP-----LK 502
 DB 385 GEDPGYTLVDSERLRLRGW-----QVPATFLGEANDIYVMRCRGFEMDPALLLE 439
 OY 503 DIRSVYQIKNKR 516
 DB 440 DYKASLKYLSDDPK 453
 RESULT 12
 DCE2_ATHH STANDARD; PRT; 494 AA.
 ID DCE2_ATHH
 AC 042472;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutamate decarboxylase 2 (EC 4.1.1.15) (GAD 2).
 GN GAD2 OR GDH2 OR ATIG65960 OR F12P19.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98363649; PubMed=9700069;
 RA Zik M., Arazi T., Snedden W.A., Fromm H.;
 RT "Two isoforms of glutamate decarboxylase in Arabidopsis are regulated
 RT by calcium/calmodulin and differ in organ distribution.";
 RL Plant Mol. Biol. 37:967-975(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=97267149; PubMed=9112779;
 RA Turano F.J., Thakkar S.S., Fang T., Weisemann J.M.;
 RT "Characterization and expression of NAD(H)-dependent glutamate
 RT decarboxylase genes in Arabidopsis.";
 RL Plant Physiol. 113:1329-1341(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gail J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Matli R., Matzball A.,
 RA Miltchev J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uutterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).

CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
 CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
 CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
 CC BIOSYNTHESIS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
 CC -----
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 CC -----
 DR EMBL: U49937; AAC31617.1; -
 DR EMBL: U46665; AAC33485.1; -
 DR EMBL: AC009513; AAF06056.1; -
 DR PIR: H96683; H96683.
 DR InterPro: IPR002129; Pyridoxal dec.
 DR Pfam: PF00282; Pyridoxal dec. 1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 DR Lyase: Decarboxylase; Pyridoxal phosphate; Calmodulin-binding;
 KM Multigene family.
 FT BINDING 276 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT DOMAIN 461 494 CALMODULIN-BINDING (BY SIMILARITY).
 SQ SEQUENCE 494 AA: 56140 MW: 741E83A250CBEC48C CRC64:
 Query Match 7.6%; Score 226; DB 1; Length 494;
 Best Local Similarity 23.0%; Pred. No. 4.8e-10;
 Matches 93; Conservative 72; Mismatches 192; Indels 48; Gaps 13;
 QY 171 NPLHDPDIPGRKIAEIRIACSLFNG---GPDSCGVNCGTRESITLACKARDLAF 226
 DB 82 NYVDMDEYPTTELRNCRVNIARLFENAPLESEFVAVGTVGSSEALMLA-----GLAF 136
 QY 227 E-----KGITPEIYAPOSAHNAFNKASFGMKIVRVLTK---MMEVDVRA 272
 DB 137 KRKMOKRKRAKSGKPRDKPNITVGANVOYCWMEKFAFYFEVLKEVNLSSGYVMDDKA- 195
 QY 273 KRAISRNTAMLCVSTPPEFPGVYIDPVPEVAKLAVK-----YKPLHVDACLGFLIVFM 326
 DB 196 -EMVDENTICVAAILGSTLNGEEDYKRLNDLVYKNEETGWNTPFIHVDAASGCFIAPFI 254
 QY 327 EKAGYPLHPDERFKGVTSISADTHKKYGAAPKSSVLVYSDKKYRNQFVDTDMOGI 386
 DB 255 ----Y-LEMDERFLPLVKSINVSCHKYGLVYAGVWVWRAEDLPELLIFHNYLGAD 309
 QY 387 YASPTIAGSRPGISAAACMAALMHGEGYVEATKQIITKTAFLKSELENIGIFVGNP 446
 DB 310 QPTFLNFSKSSQIIAYQILIRGFEQKVMNMCLENNVYLKGEIEKTERFNIYKSD 369
 QY 447 Q-LSLIAIGSRDFDI---YRLSNLTAKGWLNLQLOPPSIHFCITLLHA-----RRV 496
 DB 370 QGVPAVASLKDHSFHNFEISEMLRREGWIVPATYMPADAQH-ITVIRVAVIREDFSR 428
 QY 497 AIQFLKIDRESYTOIMKNPKAKTTGMAIYAMAQTTVRNVAEL 541
 DB 429 AERLVADISKVLHEDLTPSKIKMG-TEGIAENVKERKMEKET 472
 RESULT 13
 DEB_LISIN
 ID_DCB_LISIN STANDARD: PRT: 464 AA.
 AC Q928R9:
 DT 28-FEB-2003 (rel. 41, Created)
 DT 28-FEB-2003 (rel. 41, Last sequence update)
 DT 28-FEB-2003 (rel. 41, Last annotation update)
 DE Glutamate decarboxylase beta (EC 4.1.1.15) (GAD-beta).
 GN GADB OR LIN2463.
 OS Listeria innocua.

OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_Taxid=1642;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN-CLIP 11262 / Serovar 6a:
 RX MEDLINE-21537279; PubMed-11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetoui F., Couve E., de Darvar A., Deloux P.,
 RA Domene E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
 RA Entlan K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kunz F., Kunz F., Kurapat G.,
 RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 CC Science 294:849-852(2001).
 CC -1- FUNCTION: Converts internalized glutamate to GABA and increases
 CC the internal pH. Involved in glutamate-dependent acid resistance
 CC in gastric fluid (By similarity).
 CC -1- CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
 CC -----
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 CC -----
 DR EMBL: AL596172; CAC97690.1; -
 DR PIR: AB1740; AB1740.
 DR ListList: LIND2463; -
 DR InterPro: IPR002129; Pyridoxal dec.
 DR Pfam: PF00282; Pyridoxal dec. 1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 KM Lyase: Decarboxylase; Pyridoxal phosphate; Complete proteome;
 FT BINDING 275 275 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 464 AA: 53599 MW: 4C35CD1395ADE481 CRC64:
 Query Match 7.4%; Score 220.5; DB 1; Length 464;
 Best Local Similarity 21.2%; Pred. No. 1.2e-09;
 Matches 103; Conservative 90; Mismatches 211; Indels 81; Gaps 18;
 QY 66 LMSRKKCFKLTTRKPIIGRKIDPKLTKDDISKNSFLKVDKEYKALPSGLSSA 125
 DB 2 LYSKKNKSY-----LEPVGSSAEDR-----DIK-----YLAKEPLEPRIAYLVKDE 47
 QY 126 VLEKLEKSSMDAFQOGRASCTVYSGEKLTELLVYKAYGPAWNPPLHPDIFPLKRIE 185
 DB 48 LDEGSARONLATTFO-----TYM-EDEAKLM-----SELEKNAIDKSEYPTTABLE 95
 QY 186 AEIVYIACSLFNGGPDSS--CGCVTSGTESITL---MACK-ACRDALAFEGI---KTEPI 235
 DB 96 NRCVNIIDLVWHPADQKFMGTSTIGSSBACLGMAKFAWKRAKAEKGLDIYAKRNL 155
 QY 236 VAPQSAHAANFNKASFGMKIVRVLTKMMEVDVRAARRAISRNAMLVCSSTPPPHGVI 295
 DB 156 VTSQGYCWMEKFCYVWIDMKVYPMK-----DHQMLNTDQVLDVYDEVYIGIV 205
 QY 296 DPV-----PEVAKLAVK-----YKPLHVDACLGFLIVNEKAGYPLEHPD 338
 DB 206 GILGITYGRYDDIALALEKLEEVNSKTDYKVIHVDAASGFFPPEP-----DIWMD 260
 QY 339 FVKGVTSISADTHYGYGAPKSSVLVYSDKKYRYVQFVDPDMOGIYASPTIAGSRPG 398
 DB 261 FRLKAVISINTSGHKYGLVYRGVWLNKDESYLPELLIFKYSYLGGEPTQWQINFSRSA 320


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OY 399 GISAACMAALMHGNGCYEATKQIITKARFLKSELENIGCIFVGN--POLSLIALGSR 456
DB 321 SHIIQYNNFLRYGRFRTIHKTSVDAQYLAAVBO--TGYFDIYDNGSHLPVYCKLK 379
OY 457 D-----FDIYRLSNLMTAKMWNLNQLOPPSHHCITLLIARK-----RAIQLKARE 506
DB 380 DDANVKMTLLDLADRLQMRGMQVPAYPLPKNLNIIQRYVCRADLGFNNAEFTIOFOA 439
OY 507 SVTQI 511
DB 440 SIOEL 444

RESULT 14
DCEA_LYSMO STANDARD; PRT; 462 AA.
AC 09F5P3; 08Y9S6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN GADA OR LMO0447.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LO28 / Serovar 1/2c;
RX MEDLINE=21206233; PubMed=11309128;
RA Cotte P.D., Gahan C.G.M., Hill C.;
RT "A glutamate decarboxylase system protects Listeria monocytogenes in
   gastric fluid.";
RL Mol. Microbiol. 40:465-475(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ESD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
   Baquero F., Berche P., Blocher H., Brandt P., Chakraborty T.,
   Charbit A., Chetoui F., Couve E., de Darvar A., Dehoux P.,
   Dommann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
   Jones L.-M., Kaerst U., Krefit U., Kuhn M., Kunst F., Kurapkat G.,
   Medueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
   Nordstok G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
   Rammel B., Rose M., Schlueter T., Simoes N., Trierrez A.,
   Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RA "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Converts internalized glutamate to GABA and increases
   the internal pH. Involved in glutamate-dependent acid resistance
   in gastric fluid.
CC -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
   GAD, HDC AND TYRDC).
CC -----
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   or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF09076; AAC22560.1;
CC DR EMBL: AL591975; CAC98526.1;
CC DR PIR: AH1130; AH1130.
CC DR L1stlist: LMO00447;
CC DR InterPro: IPR002129; Pyridoxal_dec.
CC DR Pfam: PF00282; pyridoxal_dec.1.
CC DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.

```

```

KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 273 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 152 S->N (IN REF. 1).
SQ SEQUENCE 462 AA; 52498 MM; EALAA42E3EICE2RA CRC64;

Query Match 7.38; Score 218.5; DB 1; Length 462;
Best Local Similarity 20.68; Pred. No. 1,7e-09;
Matches 97; Conservative 82; Mismatches 210; Indels 83; Gaps 16;

OY 91 KLNKTRDKISKNMSEFLAVDEYKALPSOGSSSAVLEKLEYSMSMAFMEGRASGVY 150
DB 3 KTNVEQNNVPYGESE-----ESGDLPEKRNKESVDPRIAYOLVKQOLIDEGRONLA 57
OY 151 S-----GEELTFELVAKAYGDFAMSPNHPDIPGRLKAEIYRIACSLFNGCPD 201
DB 58 TFCQTYMEPEAEQIMATMEK-----NAIDSEFPQTKLSSCVNMLADIWNDES 109
OY 202 S--CGVTSGETSILMACRAC---RDALFEKGI---KTPETVAPQSAHAAPNKASY 251
DB 110 EHYWGSTVGSSEACMLGGMAMKFRWRSALKNGLDIHAKKPSLVISSGYOVCEKPCVY 169
OY 252 FGAKIVNPLTKMNEVDVRRAMRAISRNTAMLVSTQFPFGVY-----DVPPE 300
DB 170 WDIELREVPMSE-----EHLSTNTDIIIMDYVEYTIIGIIGITYGKFDIMT 219
OY 301 VAKLAVKY-----KIPLHYDACLGFLIVFMERAGVPLEHPDFRYKGVTSISADTHKY 354
DB 220 LNDLVEDYNNTHDNEVIVHDGASGAMFTPEVEG---LE--WDFRLPNVYSINTSGHKY 274
OY 355 GYAFKGSLLVYSDDKRYNTOFVDTMOGIVASPTIAGSRPGISAAACMAALMHGEN 414
DB 275 GLVYPGVGWLIMRDEKVELPELVFDVSYLGCHMPTMAINFSRASAQITIGYNNFLRFGYE 334
OY 415 GYEATKQIITKARFLKSELENT---KGIVFGN--POLSLIALGSD-----FDIYRLS 464
DB 335 GY---QIIMHRTDGAOLQSAVAETGLFEIYNDGANLPIVCKYKLDANVAANTLYDLA 390
OY 465 NLMTAKMWNLNQLOPPSHHCITLLHA-----RKRAIOLPKRIRSVQI 511
DB 391 DRLQMRGMQVPAYPLPKNLNIIQRYVCRADLGFNNAEFTIOFOA 442

RESULT 15
DCE_LYCS STANDARD; PRT; 502 AA.
AC P54767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15) (GAD) (ERT D1).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Alisa Craig; TISSUE=Pericarp;
RX MEDLINE=95284363; PubMed=7766895;
RA Gallego P.P., Whotton L., Picton S., Grierson D., Gray J.E.;
RT "A role for glutamate decarboxylase during tomato ripening: the
   characterisation of a cDNA encoding a putative glutamate
   decarboxylase with a calmodulin-binding site.";
RL Plant Mol. Biol. 27:1143-1151(1995).
CC -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
   IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
   OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
   BIOSYNTHESIS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
   GAD, HDC AND TYRDC).
CC -----

```


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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:49:49 ; Search time 29 Seconds
(without alignments)
1863.580 Million cell updates/sec

Title: US-10-053-510-8

Sequence: 1 MPSTDLMLKAFEPYLEILE.....LYSTDTVTGSGQMGSPKPH 568

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2553	85.8	568	2	JC5923 sphingosine-1-phos
2	1082	36.3	552	2	T33760 sphingosine-1-phos
3	1069	35.9	544	2	C86405 probable sphingosi
4	1008	33.9	542	2	T29835 sphingosine-1-phos
5	1007.5	33.8	589	2	S70123 sphingosine-1-phos
6	669	22.5	488	2	B69415 group II decarboxy
7	621.5	20.9	414	2	G69536 group II decarboxy
8	567.5	19.1	454	2	G72452 probable glutamate
9	549.5	18.5	473	2	G72753 hypothetical prote
10	518.5	17.4	383	2	D71084 hypothetical prote
11	514.5	17.3	384	2	G75102 group II decarboxy
12	482	16.2	363	2	E69015 glutamate decarbox
13	380	12.8	367	2	C69500 group II decarboxy
14	369.5	12.4	396	2	B64306 hypothetical prote
15	308.5	10.4	355	2	D84192 glutamate decarbox
16	261.5	8.8	466	2	B86786 glutamate decarbox
17	253.5	8.5	460	2	F70975 probable glutamate
18	242	8.1	467	2	AC1748 glutamate decarbox
19	239.5	8.0	464	2	AC3623 glutamate decarbox
20	236.5	7.9	466	1	S24234 glutamate decarbox
21	236.5	7.9	466	2	E91178 glutamate decarbox
22	236.5	7.9	466	2	F86024 glutamate decarbox
23	234	7.9	467	2	AB1379 glutamate decarbox
24	233	7.8	500	2	A48767 glutamate decarbox
25	232.5	7.8	464	2	AC1370 glutamate decarbox
26	230.5	7.7	514	2	TC9315 glutamate decarbox
27	229.5	7.7	466	1	B43332 glutamate decarbox
28	229.5	7.7	466	2	B90891 glutamate decarbox
29	229.5	7.7	466	2	G85726 glutamate decarbox

30	229.5	7.7	520	2	T49478 probable glutamate
31	228.5	7.7	496	2	T01962 glutamate decarbox
32	226	7.6	494	2	H96683 hypothetical prote
33	220.5	7.4	464	2	AB1740 glutamate decarbox
34	218.5	7.3	462	2	AB1130 glutamate decarbox
35	217.5	7.3	467	2	S75150 glutamate decarbox
36	214	7.2	475	2	T36342 probable glutamate
37	209	7.0	502	2	S56177 probable glutamate
38	204	6.9	362	2	D72734 probable histidine
39	202	6.8	39	2	G84431 probable glutamate
40	201.5	6.8	585	2	S53072 glutamate decarbox
41	198	6.7	493	2	H84431 probable glutamate
42	198	6.7	490	2	T44576 L-2,4-diaminobutyr
43	178	6.0	511	2	C5880 L-2,4-diaminobutyr
44	178	6.0	538	2	AB1855 L-2,4-diaminobutyr
45	175.5	5.9	508	2	G83977 L-2,4-diaminobutyr

ALIGNMENTS

RESULT 1									
JC5923	sphingosine-1-phosphate lyase (EC 4.-.-.) [validated] - mouse								
C:Species:	Mus musculus (house mouse)								
C:Date:	10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000								
C:Accession:	JC5923								
R:Zhou, J.; Saba, J.D.									
Biochem. Biophys. Res. Commun.	242, 502-507, 1998								
A:Title:	Identification of the first mammalian sphingosine phosphate lyase gene and 1								
A:Reference number:	JC5923; M0ID:98125521; PMID:9464245								
A:Accession:	JC5923								
A:Molecule type:	mRNA								
A:Residues:	1568 <20>								
A:Cross-references:	GB:AF036894; NID:92906010; PIDN:AAC03768.1; PID:92906011								
C:Comment:	This enzyme catalyzes the breakdown of sphingosine-1-phosphate which parti								
C:Genetics:									
A:Gene:	spl								
C:Superfamily:	sphingosine-1-phosphate lyase								
C:Keywords:	lyase								
F:42-60/Domain:	Transmembrane #status predicted <TMM>								
Query Match									
Best Local Similarity 85.8%; Score 2553; DB 2; Length 568;									
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;									
QY	1	MPSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPQMLIAMSVMVTLIVGVEYV	60						
DB	1	MPSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPQMLIAMSVMVTLIVGVEYV	60						
QY	61	FOPESLMSRKKKLFELIRKMPITGRKIEQVSKAKKDLVKNPFLKVDVYKTLPAQ	120						
DB	61	FOPESLMSRKKKLFELIRKMPITGRKIEQVSKAKKDLVKNPFLKVDVYKTLPAQ	120						
QY	121	LSSSAVLEKLEKSSMDAFQWEGRASGTYVSGEKLTELIVKAYGDFAMSNPLPIFP	180						
DB	121	LSSSAVLEKLEKSSMDAFQWEGRASGTYVSGEKLTELIVKAYGDFAMSNPLPIFP	180						
QY	181	LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTEILMACACRDLAFKIKPEIYAP	240						
DB	181	LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTEILMACACRDLAFKIKPEIYAP	240						
QY	241	AHAFAFKKASVFCMKIVRPLTMMVDVAMRAISRNAMLVCSVPDPHVDIVPE	300						
DB	241	AHAFAFKKASVFCMKIVRPLTMMVDVAMRAISRNAMLVCSVPDPHVDIVPE	300						
QY	301	VALAVKRYIPLHVDACLGFLIVEMKAGYPLEHFPDFRVKCVTSISADTHKYYAPK	360						
DB	301	VALAVKRYIPLHVDACLGFLIVEMKAGYPLEHFPDFRVKCVTSISADTHKYYAPK	360						
QY	361	SSVLVYSDKKRYNYQFFVDWOGGIYASPTAGSRPGISACMAALMHFGNGVEAT	420						
DB	361	SSVLVYSDKKRYNYQFFVDWOGGIYASPTAGSRPGISACMAALMHFGNGVEAT	420						

Db 543 QY 544

RESULT 4

T29835

sphingosine-1-phosphate lyase (EC 4.-.-) B0222.4 [similarity] - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T29835

R:Du, Z.; Gattung, S.

submitted to the EMBL Data Library, February 1996

A:Description: The sequence of *C. elegans* cosmid B0222.

A:Reference number: Z20696

A:Accession: T29835

A:Status: preliminary; translated from GB/EMBL/DDBU

A:Molecule type: DNA

A:Residues: 1-542 <DU>

A:Cross-references: EMBL:U50312; PIDN:AAA92321.1; CESP:B0222.4

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:B0222.4

A:Introns: 50/71; 74/3; 223/2; 468/2

C:Superfamily: sphingosine-1-phosphate lyase

C:Keywords: lyase

Query Match 33.9%; Score 1008; DB 2; Length 542;

Best Local Similarity 38.1%; Pred. No. 1e-70;

Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

QY 19 LEVYSTRKANVNGHCTKPEWQILMSVYVLLIYWGVEFVQPELSMRKKCKEKL 78
 Db 5 LEQYHS-ARDLLFEELKRPILVSVSTIATVTLNLRHMLDENGIRKRLSTWETTV 63
 QY 79 RKMPITGRIQDKLNTKDKISNMFVLYKDYVALBPQGLSSSAVLEKLEYSMDA 138
 Db 64 KRPFIRKIMIDQLNEVKOLEKSLRIYVSTETFTIPSHVGRTEVLAAYDDLEG 123
 QY 139 -FMQGRASGVYSGEKL--TELLKAYGDFAMSNPLHPIFGRLKIEAIVRIACSL 195
 Db 124 PAFLEGRVSGAVYNNRDEDDEREMVEYVCKFAWTPNLPKLFPGVRIKMAEYVRCNM 183
 QY 196 FNGSPDSCGVYSGTESILMACACRDIAFEKGIKTPETLVAPOSAHAENKASYFGMK 255
 Db 184 MNDSETCGTMSYSGSISILLACLAHRNRLKRGEXYTEMIVPSVHAFAEFCFRK 243
 QY 256 IYVAVPLTKM-MEVDVAMRAISRNTAMLVCSFPORPHGYIDVPEVAKIAYKIPLV 314
 Db 244 VKRIPVDVPEYKVDLKKMAALNKRTCMVGSAFNPFGTVDDIEAIGQLEVDIPVHV 303
 QY 315 DACLGFLIVFMKAGYPLEHPDFVKGVTISADTHKYGAVAPKSGSLVLYSDKKYRNY 374
 Db 304 DACLGFLPLPLEED---EIRYDFVPGVSSISASSHKGLAPKSSVLYLNKELHN 359
 QY 375 QRFVDTWOGGIIASPTIAGSRPGGISAACMAALMHGNGEYVETAKOIKTARFLKSEL 434
 Db 360 QYFCADWOGGIIASPTIAGSRPGGISAACMAALMHGNGEYVETAKOIKTARFLKSEL 419
 QY 435 ENIKGIFVGNPQLSLIAGSRD-FDIYRLSLMTAKGWNLOLOPPSIHFCITLLHAR 493
 Db 420 SNIKGIRKLOGPSVNCIVSWTTNDGVELYRFHNMKEHWMOLNOLPAGCHIVATNMHTH 479
 QY 494 KRYAIOFLKDIRSVTQIM--KNPKAKTTGMAIYMAQTVVIRNMVAELSLFELSLYS 551
 Db 480 PGAAEAFVADCRAAVEFVSKRPSKESDKTSEAIYGLAOSIPRSLVHERFAHYIDAVYA 539

RESULT 5

S70123

sphingosine-1-phosphate lyase (EC 4.-.-) [similarity] - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein D9819.5

C:Species: *Saccharomyces cerevisiae*

C:Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S70123

R:Fullton, L.

Submitted to the EMBL Data Library, May 1996

A:Description: The sequence of *S. cerevisiae* cosmid 9819.

A:Reference number: S70114

A:Accession: S70123

A:Molecule type: DNA

A:Residues: 1-589 <FUL>

A:Cross-references: EMBL:U51031; NID:g1332635; PIDN:AAB64470.1; PID:g1230658; GSPDB:G

C:Genetics:

A:Gene: SGD:DP1; MIPS:YDR294C

A:Cross-references: SGD:S0002702

A:Map position: 4R

C:Superfamily: sphingosine-1-phosphate lyase

C:Keywords: lyase; transmembrane protein

F;60-72/Domain: transmembrane #status predicted <TM>

Query Match 33.8%; Score 1007.5; DB 2; Length 589;

Best Local Similarity 39.1%; Pred. No. 1.2e-70;

Matches 209; Conservative 108; Mismatches 185; Indels 33; Gaps 12;

QY 51 LLIVMGYEF-----VFQPESL----WSRRKKCKEKLTKRMPITGRIQDKLNTK 97
 Db 60 LEVIFCYKLISNFFYLKTVGPVRLAVRYTEHSSRLRFLWLDSPFLRGTEVEYKVKQ 119
 QY 98 DISKNSFLVKDEYVK--ALPSQGLSSSAVLEKLEYSMDA--DAFMQGRASGVYSGE 153
 Db 120 SIDEL--IRSDQLMNFQPLPSNGIPDQDVEIELKLNLDLHTQKBEKVGAYHGG 177
 QY 154 EKLTELLKAYGDFAMSNPLHPIFGRLKIEAIVRIACSLFNGSPDS--CGCVTSGETE 212
 Db 178 DDLIHQTIAYEKYCVANQLPDPVFAVRKMESEVSMVLRFNAPSDDTCGTTSGTE 237
 QY 213 SLIMACKACRDIAF-EKGIKTPETLVAPOSAHAENKASYFGKIVAVPL-TKMEVDVR 270
 Db 238 SILLACISAMVYLHNGHTEPELIAVTAHAFDAAYFGKILRVELDPTTYQVDLG 297
 QY 271 AMRAISRNTAMLVCSFPORPHGYIDVPEVAKIAYKIPLVADACLGFLIVFMKAG 330
 Db 298 KYVKFKINKTILLVGSAPNPHGIIADDELGIAOKYKPLVAVDSLSFYISPMKAG 357
 QY 331 YPLEHPDFVKGVTISADTHKYGAVAPKSGSLVLYSDKKYRNYQRFVDTWOGGIYASP 390
 Db 358 YKMLPLDFFRVPTVSTISCTHKGFAPKSSVIMYVNSDLRMHQYVYVNPAMTGGLYGSP 417
 QY 391 TINGSPDSCGVYSGTESILMACACRDIAFEKGIKTPETLVAPOSAHAENKASYFGMK 449
 Db 418 TLGASRGALVGCWMTVMNGENGYESQETIVGAAMKFKKTYIOENIPDLNIMGNPRYS 477
 QY 450 LIALGSRDPIYRLSLMTAKGWNLOLOPPSIHFCITLLHARKRYAIOFLKDIRSVT 509
 Db 478 VIFSSSKTLINHELSDRLSKKGNHFNALOKPVALHMAFRLSLAH---VVDEICDILRTTV 534
 QY 510 QIMK---NPKAKTTGMAIYMAQTVVIRNMVAELSLFELSLYS 557
 Db 535 QELKSESNSKPSDGTSGALYGVAGSVYTAGVADKLIVGFIDALYKLPGEDETATK 589

RESULT 6

B69415

group II decarboxylase homolog - *Archaeoglobus fulgidus*C:Species: *Archaeoglobus fulgidus*

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999

C:Accession: B69415

R:Kient, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

Glodek, A.; Zhou, L.; Overbeek, R.; Goeyne, N.H.; Sutton, G.G.; Gill, S.; Kikness, E

Nature 390, 364-370, 1997

A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kalne, B.P.; Sykes,

Smith, H.O.; Moese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; WUID:98049343; PMID:9389475

A:Accession: B69415

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-488 <KLE>
A:Cross-references: GB:AE001012; GB:AE000782; NID:g2689335; PIDN:AA89922.1; PID:g264925
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 22.5%; Score 659; DB 2; Length 488;

Best Local Similarity 36.5%; Pred. No. 2.8e-44;

Matches 155; Conservative 83; Mismatches 171; Indels 16; Gaps 8;

```
OY 92 LNKRTDDISKNNMSFLKVDKEYKALPSQGLSSAVLEKLEKSSMDAFQEGRASGV-Y 150
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 LNKGNHNSFEYKIRITTKIMSPN-GSDAEGVLEKLEKEDYAKNDPEPHSRMGHITY 68
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 151 SGEKLTLLVAYGDFAMSNPLHPDIPFRLKIEAIVRIACSLFNGGPPSCCGTSGG 210
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 AGLKQVLELARKAYLMYDKMTMLDPTCPPLRMREVRMASSLLNDEEVYNGFTYGG 128
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 211 TESTIMACKACRDIAFEK---GKTPETVAPQSAANAANKASVGMKIVAPLTKMMEV 267
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 TESTIMALKARE-KERREGNNVPELVLPATAPRAVKSLEYKMRCLRAKLDDELRA 187
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 268 DVAMARRAISNTALVCTFOPPHGVIDPVEVAKLVKKYKPLHVDACLGELIVEME 327
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 DVEYKELVGDKTAMIVASAPNYPGVDDIKALSDIADVGLWHLVDACLGELHFFR 247
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 328 KAGVLEHPDFPRKGVTSISADTHKYGTAAPKSSLVLSDKKRNYPFVDTMOGITY 387
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 ELGEEKIP-DPFSVEGVHSISADFHKYGSLSPGASVILYRNKAKLEGOIFVAVSWPGYPL 306
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 368 ASPTAGSRPGISAAQAAALMHGENGVEATKQIITARLKELEINIGIFVFGPQ 447
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 VNTAVALSTRAGTLLAAAVMSYLSGDFGLTKAKTLVAKKRLDGLTEL-GLLELGSPE 365
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 448 LSLALGSRDPDIYRLSNLMTAKGMNL-----NOLQPPSIHFCITLLHARKRAVLOFL 501
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 366 GAVLAFTSEBRNHLFEVSTLMAEKGMVYQSPGSKTLGPRSLHFEVITIGHA--EYVDEFL 423
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 502 KDIRE 506
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 424 EDMRE 428
```

RESULT 7

659536
Group II decarboxylase homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999

C:Accession: G69536

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A:Authors: Ulteback, T.; Cotton, M.D.; Spriggs, T.; Artlisch, P.; Kane, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: G69536

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-414 <KLE>
A:Cross-references: GB:AE000946; GB:AE000782; NID:g2689269; PIDN:AA88962.1; PID:g264822
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 20.9%; Score 621.5; DB 2; Length 414;

Best Local Similarity 38.6%; Pred. No. 1.1e-40;

Matches 153; Conservative 68; Mismatches 152; Indels 23; Gaps 9;

```
OY 126 VLEKKEYSMDAFQEGRASGVY-SGEKLTLLVAYGDFAMSNPLHPDIPFGLKI 184
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 VLSLEKASEDLNERTGRLEFAYVETGDNIRKAKALVFAEKNLIDFVFSAVFF 65
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 185 EAEIVRIACSLFNGGPPSCCGTSGTSTIMACKACRDIAFEK--GKTPETVAPQSAH 242
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
DB 66 EKEVGFARNLMHGDA-AVSGFTFGCTSIMLAVKAADYRKKECTAEVPEILLPISIH 124
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 243 AAFNKAASYFGMKIVRVPLTKMMEVDVAMRAISRNTAMLVCSPPPHGVIDPVEVA 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 PAFLLKAAVYLGKAVRLVY-KDAKGDVDAFAEAVSGKATALLASAPNPFGTIDPEVETIA 183
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 303 KLVAKYKILPHVDACLGELFVEMKAGYPLEHPDFPRKGVTSISADTHKYGTAAPKSS 362
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 EIAAERNVLLHVDACLGELFVEMKAGYPLEHPDFPRKGVTSISADTHKYGTAAPKSS 242
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 363 LVLYSDKKYRNQFVPDVMOGGIYASPTIAGSRPGISAAQAAALMHGENGVEATKQ 422
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 VLFERDAELKCSMFVDVTSFGYFVNOAVLSSRPEGFLAAFAVITKLGVBGKELASK 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 423 IY---KTARFLKSELENIGKIFVGNPOLSLIALGSRDPDIYRLSNLMTAKGMNL-- 475
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 303 ILSARDKIYRGLKS-----LGFESVGEVSSVLAMTNDVDLGMFVNMMKRLGMQLHOK 357
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 476 ---QLQPPSIHFCITLLHARKRAVLOFLKDIREV 508
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 GLKEVDIPDNHILTLSPVH--DGVAKEFEVDAKAL 391
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 8

672452
Probable glutamate decarboxylase APE2267 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G72452

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hakiawa, Y.; Jin-no, K.; Tanaka, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: G72452

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-454 <KAM>

A:Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BA81279.1; PID:g5105968

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2267

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 19.1%; Score 567.5; DB 2; Length 454;

Best Local Similarity 35.2%; Pred. No. 2.1e-36;

Matches 139; Conservative 74; Mismatches 167; Indels 15; Gaps 9;

```
OY 126 VLEKKEYSMDAFQEGRASGVY-SGEKLTLLVAYGDFAMSNPLHPDIPFGLKI 184
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 VVRLAEIRAMDAREGGKLFYLYETGDPGVKEVSLRAFEKFLDTNLDPTVRSALFF 63
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 185 EAEIVRIACSLFNGGPPSCCGTSGTSTIMACKACRD-LAFKGIKTELPVAPQSAHA 243
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 EBEIVSPASSLAGVGVGVYTGTTGTSIIILAAVAAHEWYKSLGSRTPGVAVQYVHP 123
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 244 AFNKAASYFGMKIVRVPLTK-MMEVDVAMRAISRNTAMLVCSPPPHGVIDPVEVA 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 SVRKAARYLGMRLSTAPVDPGSKRVDISLVLYDDRTAMVAVSAPNYPGVTDVRSVA 183
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 303 KLVAKYKILPHVDACLGELFVEMKAGYPLEHPDFPRKGVTSISADTHKYGTAAPKSS 362
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 EALSQQRWLHVDACVGGFLTFEKRLEGL-YSGAFAPVEGVYSMDLHKIGTSPKAS 242
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 363 LVLYSDKKYRNQFVPDVMOGGIYASPTIAGSRPGISAAQAAALMHGENGVEATKQ 422
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 VLFERDGLSKKHSIFADLRWPGYPIINTVILSSRSVAPLAAMAVTNTLGRGVELARK 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 423 IKTARFLKSELENIGKIFVGNPOLSLIALGSRD-FDIYRLSNLMTAKGMNLQ--- 478
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 303 AVEARDEIMRGLESI-GPRLAPRIESTILSVLADPADTLRPHANMSRGMWLG-LQPGV 360
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 479 ---PPPSIHFCITLLHARKRAVLOFLKDIREVTO 510
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

DB 361 EGIAPPNIHLTSPH--KLVSPOFLGDARASSSE 393

RESULT 9

G72753 hypothetical protein APE0020 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G72753
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72753

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-473 <KAW>
A:Cross-references: DDBJ:AP000058; NID:95103388; PIDN:BAA78929.1; PID:95103408

A:Experimental source: strain K1
C:Genetics:

A:Gene: APE0020
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 18.5%; Score 549.5; DB 2; Length 473;
Best Local Similarity 34.4%; Pred. No. 5, 8e-35;

Matches 135; Conservative 70; Mismatches 173; Indels 15; Gaps 8;

QY 126 VLEKLEKSSMDAFOGRASGTYS-GEEKLTLLVKA YGDFAMSNPLHPDIFPGLRKI 184
DB 13 VIRELFLLSSRDINPWTGRVTHVYDPCMDVKKASKALELYRDKTMDLDFYVPSIIEI 72

QY 185 EAEIVRIACSLNNGSGDSCGVTSGTSESLMACRCRLAFKGIK-TPETIAPQSAHA 243
DB 73 EKQLLGFAHLTHAPBEGYSGTFTYGGTESIIIAVLAARERWRAGSGAGKIMPTIAPH 132

QY 244 AENKASVYGMKIVRYPLTKM-MEVDVRRARRAISNTAMLCSTQPFPHGVIDPPEVA 302
DB 133 AFKAKAYLLGKVERPVPDSVTLQADPAIEEKIDDTYMTIVASANDPYGSLDPEDIG 192

QY 303 KLAIVKIKPLHVDACIGFLIVFMKAGYPLEHPDFRVKGYVTISADTRKGYADKSS 362
DB 193 DIAAARDVWLHVDACIGVLAFAASDAGEV-GKFDGVEGYRFSVDMHKGYAPAKGSS 251

QY 363 LVLYSDKKRYNQFPVDTMOGIVASPTIAGSRPGISAAACAAALMHGNGCYVATNQ 422
DB 252 ILLFRARDKKPTIEVDSSMPGPIVNOAILSTRSAGTLAAAVARTLGVEGYRELGM 311

QY 423 IIKTARFLKSELENIGIFVGNPQSLIALSGRDFDIYRLSNLMTAKGNLNLQD---- 478
DB 312 VLEARRRIGKLESL-GLEVLGRPKGILISFTSDSDIDVVEVATRLGRAGM-VVQLDPPMK 369

QY 479 ---PPSHIFCITLLHARRVAIOFLKIDRESV 508
DB 370 HLGFTSIHLTSPHIA--RVVDSFLAAVEESI 400

RESULT 10
D71084

hypothetical protein PH0937 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C:Accession: D71084
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Sekita

M.; Ohikubo, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71084

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-383 <KAW>

A:Cross-references: GB:AP000004; NID:93236131; PIDN:BAA30034.1; PID:93257351

A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by Genba

C:Genetics:
A:Gene: PH0937

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 17.4%; Score 518.5; DB 2; Length 383;
Best Local Similarity 31.1%; Pred. No. 1, 1e-32;

Matches 123; Conservative 83; Mismatches 165; Indels 25; Gaps 7;

QY 117 PSQGLSSAVLEKLEKSSMDAFWQGRASGTYSGEELKTELIVKAYGDFAMSNPLHPD 176
DB 4 PRIGLPEKVEVIELINEKTKKDLTFSSGKILGSMCTMPH---DLAIEVYTKYIDRNIGDGC 60

QY 177 IEPGLKIEAEIVRIACSLFNGPDSGCGVTSGTSESLMACACADLAFKGIKTPETV 236
DB 61 LHGCTRIEEVEVTEMSDILH-LEKGHIVSGGTETANILAVAFENLS---DVEKPELI 116

QY 237 APOSAAAFNKAASYGMKIVRYPLTKMMEVDVRRARRAISRTAMLCSTQPFPHGVID 296
DB 117 LRKSAHFSTIKAGEMGLVMAELNPDVTVDVRYDEAKISDNTIGIVGAGTGLGYVD 176

QY 297 PVPEVAKLAVKXKIPLDVACIGFLIVFMKAGYPLEHPDFRVKGYVTISADTRKGY 356
DB 177 DIPALSDLRDYGIPLDVDAAFGFIYIPPAKELGYELP-DFDKLKGVSITIDPRKMG 235

QY 357 ARKSSLVLYSDKKRYNQFPVDTMOGIVASPTIAGSRPGISAAACAAALMHGNGCY 416
DB 236 APVPAGIVFRRKKYKALSVLAAPYLAGKQWQATITGRPGASVIAVWALKLHGEFG 295

QY 417 VEATKOIITARFLKSELENIGIFVGNPQSLIALSGRDFDIYRLSNLMTAKGNLN- 475
DB 296 MRIVERAMLSRFAEIKINNAMLVREPMINIVFQIK--NLKVERELKSRGICSA 353

QY 476 ----QLQPPSHIFCITLLHARRVAIOFLKIDRE 506
DB 354 HRCYIRIVFMP-----HVTREMEIEFLDKLE 380

RESULT 11
G75102

group II decarboxylase PAB1578 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G75102
R:anonymous, Genoscope

A:Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s

A:Reference number: A75001
A:Accession: G75102

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-384 <KAW>
A:Cross-references: GB:AJ248286; GB:AL09836; NID:95458366; PIDN:CAB50124.1; PID:9545

A:Experimental source: strain Orsay
C:Genetics:

A:Gene: PAB1578
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 17.3%; Score 514.5; DB 2; Length 384;
Best Local Similarity 30.6%; Pred. No. 2, 3e-32;

Matches 121; Conservative 86; Mismatches 164; Indels 25; Gaps 7;

QY 117 PSQGLSSAVLEKLEKSSMDAFWQGRASGTYSGEELKTELIVKAYGDFAMSNPLHPD 176
DB 5 PERGLPREVNLNLEDKTVVDLTFSSGKILGSMCTMPH---ELAIEVFARYIDRNIGDGC 61

QY 177 IEPGLKIEAEIVRIACSLFNGPDSGCGVTSGTSESLMACACADLAFKGIKTPETV 236
DB 62 LHPGTRKIEEVEVTEMSDILH-LEKGYHIVSGGTETANILAVAFENIS---DAERPELI 117

QY 237 APOSAAAFNKAASYGMKIVRYPLTKMMEVDVRRARRAISRTAMLCSTQPFPHGVID 296

Db 118 LPKSAHSEFKIAGSLGKLVKMAELKODYADVADKVEAKISDNTIGIAGTGLGVVD 177
QY 297 PVPEVAKLAVKRYKIPMLHVDACTGLFLVFMKAGYPLEHPDPFRKGVTSISADTHKGY 356
Db 178 DIPALSDARXGIFPLHVDAFGFVIFPAKSLGVDLP-DDEFLKGVESTITIDPHKGM 236
QY 357 APKSSLVYSDKKYRNYQFVDTDWOGGIYASPTIAGSRPGGISACMAALMHFGNGY 416
Db 237 APIPAGGIIFRRKKYLAISVLAAPYLAGKVMQATITGTIRPGASVLAVALIKHLGFEY 296
QY 417 VEARKQIITKARFLKSELENKGIYFVGNPQSLIALGSRPDIYRLSNLMTAGWNLN- 475
Db 297 REIVKAMWELSRWAEIKKLNAMLVREPLNIVSFQTK--NLKVERELKRGWGISA 354
QY 476 -----QLOPPSIHFCITLLHARRVAIQFLKDI 506
Db 355 HRCYIRIVFMP-----HVTKEWVEFLDLRE 381

RESULT 12

E69015

glutamate decarboxylase - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 22-Jun-1999

C:Accession: E69015

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Kl, S.; Church, G.M.; Vitcare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Residues: 1-363 <MTH>

A:Molecule type: DNA

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Cross-references: GB:AE000881; GB:AE000666; NID:92622206; PID:AA85605.1; PID:9262221

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH116

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 16.2%; Score 482; DB 2; Length 363;
Best Local Similarity 32.1%; Pred. No. 7.5e-30;
Matches 117; Conservative 77; Mismatches 159; Indels 12; Gaps 8;

QY 140 WQEGRAGTYVSGEKLTELIVKAYGDFAMSNPLHPDIFPGLRIEAIYIACSLFNGG 199
Db 3 YTSRIIGSMCTSSHPILAR---RYVCDPLESNLDGDFLFRGTRELESGVIGMLGELS-E 58
QY 200 PDSCGCVTSGGTESILMACACRDIAFEKIGTPEIYVAPQSAHAFAFKKASVFGMKIVRV 259
Db 59 PDAGHITIGTGTENLAKMARARMA--GAKEPEIIVPKSAHSPFRKAADILRLREA 115
QY 260 PLTKMMEVDVYRAMRATSRNTAMLCSTPQEPHGVDPVPEVAKLAVKRYKIPMLHVDACTGL 319
Db 116 ELDDYDVADVESYAKLLISENTVAAGVAGTTELRIDPVEELSEICLDEDIHLHIDAAG 175
QY 320 GFLIVMEKAGYPLEHFEFRVGVTSISADTHKGYAPKSSVLVSDKKYRNYQFVD 379
Db 176 GFLIFLRETAGALPE-FDKRLGCVSSITVDPHKMGIALIPSGCILFRDASVLD-ANSIE 233
QY 380 TDMOGGIYASPTIAGSRPGGISACMAALMHFGNGYVEATQIITKARFLKSELENK 439
Db 234 TPYLETKQOS-TIVGTRTGASAAATWAIMKMGREGYRKLALRYMGVTRRLRDGLVELDY 292
QY 440 IFVGNPQSLIALGSRPDIYRLSNLMTAGWNLNLOPPSIHFCITLLHARRVAIQ 499
Db 293 QLVV-EPELNTIVANHPAMGPHIELRLLEELGMAVSVSCPPAIR-VLMPHIMEHIEL 350
QY 500 FLKDI 504
Db 351 LRLDL 355

RESULT 13

C69500

group II decarboxylase homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999

C:Accession: C69500

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Overbeek, T.; Cotton, M.D.; Springs, T.; Artlich, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: C69500

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-367 <KLE>

A:Cross-references: GB:AE000964; GB:AE000782; NID:92689287; PID:AA869250.1; PID:9264

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 12.8%; Score 380; DB 2; Length 367;
Best Local Similarity 27.7%; Pred. No. 7.1e-22;
Matches 108; Conservative 80; Mismatches 164; Indels 38; Gaps 11;

QY 126 VLEKIKREYSSMDAFWQEGRAGTYVSGEKLTELIVKAYGDFAMSNPLHPDIFPGLRIE 185
Db 3 IIEELRAVRENDIYRSLVSMCTVP-----HPVAVEAHRHFTETNLDGDFIFRGYVELE 57
QY 186 AEIVRIACSLFNGGPDSC---GCVTSGGTESILMACACRDIAFEKIGTPEIYVAPQSA 241
Db 58 AKIRLIGDILH-----CEPAGYICSGGTETANIGIARARNVQK--ENPNIVIPKTA 109
QY 242 HAANKKASVFGMKIVRPLTKMMEVDVYRAMRATSRNTAMLCSTPQEPHGVDPVPEVAKLAVK 301
Db 110 HFSEKIGDILGVYIKRAGVDEEYKVDGVEDLDEVTVAIVIAGTTELGQIDPVEL 169
QY 302 AKLAVKRYKIPMLHVDACTGLFLVFMKAGYPLEHFEFRVGVTSISADTHKGYA--PK 359
Db 170 SKLAEHQVELHVDAAGGLVIFPMDN-----PYFPDQNGVGSITIDPHKMGATIPA 224
QY 360 GSSVLVYSDKKYRNYQFVDTDWOGGIYASPTIAGSRPGGISACMAALMHFGNGY 416
Db 225 GGII-----FRNESYLALEVEETPYLSTQFTLGTIRPGTGVASAVAKSLGFGEM 277
QY 417 VEARKQIITKARFLKSELENKGIYFVGNPQSLIALGSRPDIYRLSNLMTAGWNLN- 475
Db 278 REVVKNCCKNTRLIVEEKRD-LGEPVIEPVANVSP--RTDEARKIEELYRMRVIST 334
QY 477 LQPPSIHFCITLLHARRVAIQFLKDI 506
Db 335 IREPKAIRF-VVMPHVTVEEVIKNIISDFRK 363

RESULT 14

B64306

hypothetical protein M0050 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Jun-1999

C:Accession: B64306

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: B64306

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-396 <BDL>

A:Cross-references: GB:067463; GB:L77117; NID:g1590846; PIDN:AAB98031.1; PID:g1498811; C:Genetics;
A:Map position: REV52237-51047
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 12.4%; Score 369.5; DB 2; Length 396;
Best Local Similarity 27.9%; Pred. No. 5,3e-21;
Matches 103; Conservative 82; Mismatches 139; Indels 45; Gaps 13;

QY 113 VVALPQGLSSAVLEKLEKEYSSMDAFWQDGRASGVYSGEKLTELKVAAYDFAKSNP 172
DB 1 MRNMQEKGSEKLELEKLYRSLDLKYEENIFGSCSNVLPITRITVDI---FLETNL 57
QY 173 LHPDIFPGKRIAEIVRIACSLFNGDSCGCVTSGTESILMACKACDLAEKGRK 231
DB 58 GDEGLKRGKRLLEKKAVALIGSLN-NKDAIGHIVSGGTANMALFCITNIREKRRKG 116
QY 232 ----TPEIVAPQSAHAFAFNKAASYGKMLVRVPLTKMMEVDVAMRAISR---NTAML 283
DB 117 LSKNEHPKILVPTAHSPFEKREMMDELYIAPIKEDYTIDEKPVKDAVEDYDVGIIIG 176
QY 284 VCSTPOPGVIDPVEVAKLAVKIKIPLHVDACLGGLIVME---KAGYPLEHPDF 339
DB 177 IAGTTEL--GTIDNIELSKIAKENNIIYHVDAAFGLVLPFLDDKXKKKG--VNYKFD 232
QY 340 RVKGVTSISADTKHYGAPKSSLVLYSDKKYRNYOFEVPTDMOGGIYASP-----T 391
DB 233 SL-GVDSITIDPKMKHCPSPSGILFKDIGKRY---LDV-----APYLETRQAT 281
QY 392 IAGSRPGISAAACWALMHFENGVEATKQIKITAFKSELE--NKGIFVEGNPOLS 449
DB 282 ILGTRVGFAGCACTYAVLRVYRGQRKIVNECMENLTYLKILKENNFKVI---EPILN 338
QY 450 LIALGSRDF 458
DB 339 IVAIEDEY 347

RESULT 15

glutamate decarboxylase [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84192
R:Ng, W.V.; Kennedy, S.P.; Mahairs, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leitauer, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freltas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: AB4160; MUID:20504483; PMID:11016950
A:Accession: D84192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <STO>
A:Cross-references: GB:AE004437; NID:g10579954; PIDN:AAG18904.1; GSPDB:GN00138
C:Genetics:
A:Gene: gad

Query Match 10.4%; Score 308.5; DB 2; Length 355;
Best Local Similarity 27.5%; Pred. No. 2.6e-16;
Matches 94; Conservative 64; Mismatches 155; Indels 29; Gaps 9;

QY 167 FANSNPLHPDIFGLKIEAEIVRIACSLFNGDSCGCVTSGTESILMACKACDLAF 226
DB 35 FLATNPDDPTPYAVARERDAVALIGEIV-GLSSPHGYIAGGTENALQAVRAARNRAD 93
QY 227 EKGITPEIYAPQSAHAFAFNKAASYGKMLVRVPLTKMMEVDVAMRAISRNTAMLYCS 286
DB 94 ADAV---NVYAPASAHSPFOKADYLGVELRLAPTDGDRADVAADVADYDGTAVYGV 150
QY 287 TPQFPGVIDPVEVAKLAVKIKIPLHVDACLGGLIVFMEKAGYPLEHPDFRKGVS 346

DB 151 AGTTEYGRVDPILALDIAGVDANLHVDAAMGFVLPF-----TDHDMSEADAPVNT 203
QY 347 ISADTKHYGAPKSSLVLYSDKKYRNYOPE---FVDTDMOGGIYASPTIAGSRPGISA 402
DB 204 MALDPHMGAPVPAGGFLARDEPIDALAEITPYLESDT-----PTLGTRSGAGVA 257
QY 403 ACWALMHFENGVEATKQIKITAFKSELENIGIFVFGNPOLSLIALGSRDPDIYR 462
DB 258 GALASLRALMPDGYREYERTGNAEYLAELA-ARGYDVY-DPELPVLAADPDADFAQA 315
QY 463 LSNLMTAKGNLNOLOFPSPSIHFCITLLHARKKVAIOFLKDI 504
DB 316 LRE-----EGWRISRTASDALRVVCMF--HYTREMLAFLDDV 351

Search completed: October 6, 2003, 13:56:25
Job time: 31 secs

